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(71) Applicant (for all designated States except US):	CURAGEN CORPORATION [US/US]; 555 Long Wharf Drive, 11th floor, New Haven, CT 06511 (US).			
(72) Inventors; and				
(75) Inventors/Applicants (for US only):	GERLACH, Valerie, L. [US/US]; 18 Rock Pasture Road, Branford, CT 06405 (US). MACDOUGALL, John, R. [CA/US]; 117 Russell Street, Hamden, CT 06517 (US). SMITHSON, Glennida [US/US]; 125 Michael Drive, Guilford, CT 06435 (US). MILLET, Isabelle [FR/US]; 74 Carrington Avenue, Milford, CT 06460 (US). STONE, David [US/US]; 223 Whitehorn Drive, Guilford, CT 06437 (US). GUNTHER, Erik [US/US]; 34 Bryan Road, Branford, CT 06405 (US). ELLERMAN, Karen [US/US]; 87 Montoya Drive, Branford, CT 06405 (US). GROSSE, William, M. [US/US]; 15 Rice Terrace Road, Apartment C, Branford, CT 06405 (US). ALSO BROOK, John, P., II [US/US]; 60 Lake Drive, Madison, CT 06443 (US). LEPLEY, Denise, M. [US/US]; 51 Church Street, Branford, CT 06405 (US). BURGESS, Catherine, E. [US/US]; 90 Carriage Hill Drive, Wethersfield, CT 06109 (US). PADIGARU, Muralidhara [IN/US]; 71 Hampton Park, Branford, CT 06405 (US). KEKUDA, Ramesha [IN/US]; 1 Malthy Street, Branford, CT 06405 (US). SPYTEK, Kimberly, A. [US/US]; 28 Court St. #1, New Haven, CT 06511 (US). LEACH, Martin, D. [GB/US]; 131 Beechwood Drive, Madison, CT 06433 (US). SHIMKETS, Richard, A. [US/US]; 191 Leete Street, West Haven, CT 06516 (US).			
(74) Agent:	ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).			
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(54) Title: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

(57) Abstract: Disclosed herein are nucleic acid sequences that encode novel polypeptides. Also disclosed are polypeptides encoded by these nucleic acid sequences, and antibodies, which immunospecifically bind to the polypeptide, as well as derivatives, variants, mutants, or fragments of the aforementioned polypeptide, polynucleotide, or antibody. The invention further discloses therapeutic, diagnostic and research methods for diagnosis, treatment, and prevention of disorders involving any one of these novel human nucleic acids and proteins.

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NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

FIELD OF THE INVENTION

The invention generally relates to nucleic acids and polypeptides encoded thereby.

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BACKGROUND OF THE INVENTION

The invention generally relates to nucleic acids and polypeptides encoded therefrom. More specifically, the invention relates to nucleic acids encoding cytoplasmic, nuclear, membrane bound, and secreted polypeptides, as well as vectors, host cells, antibodies, and recombinant methods for producing these nucleic acids and polypeptides.

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SUMMARY OF THE INVENTION

The invention is based in part upon the discovery of nucleic acid sequences encoding novel polypeptides. The novel nucleic acids and polypeptides are referred to herein as NOVX, or NOV1, NOV2, NOV3, NOV4, NOV5, NOV6, NOV7, and NOV8 nucleic acids and polypeptides. These nucleic acids and polypeptides, as well as derivatives, homologs, analogs and fragments thereof, will hereinafter be collectively designated as "NOVX" nucleic acid or polypeptide sequences.

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In one aspect, the invention provides an isolated NOVX nucleic acid molecule encoding a NOVX polypeptide that includes a nucleic acid sequence that has identity to the nucleic acids disclosed in SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26. In some embodiments, the NOVX nucleic acid molecule will hybridize under stringent conditions to a nucleic acid sequence complementary to a nucleic acid molecule that includes a protein-coding sequence of a NOVX nucleic acid sequence. The invention also includes an isolated nucleic acid that encodes a NOVX polypeptide, or a fragment, homolog, analog or derivative thereof. For example, the nucleic acid can encode a polypeptide at least 80% identical to a polypeptide comprising the amino acid sequences of SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 27. The nucleic acid can be, for example, a genomic DNA fragment or a cDNA molecule that includes the nucleic acid sequence of any of SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26.

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Also included in the invention is an oligonucleotide, e.g., an oligonucleotide which includes at least 6 contiguous nucleotides of a NOVX nucleic acid (e.g., SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26) or a complement of said oligonucleotide.

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Also included in the invention are substantially purified NOVX polypeptides (SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 27). In certain embodiments, the NOVX polypeptides include an amino acid sequence that is substantially identical to the amino acid sequence of a human NOVX polypeptide.

5 The invention also features antibodies that immunoselectively bind to NOVX polypeptides, or fragments, homologs, analogs or derivatives thereof.

In another aspect, the invention includes pharmaceutical compositions that include therapeutically- or prophylactically-effective amounts of a therapeutic and a pharmaceutically-acceptable carrier. The therapeutic can be, e.g., a NOVX nucleic acid, a NOVX polypeptide, 10 or an antibody specific for a NOVX polypeptide. In a further aspect, the invention includes, in one or more containers, a therapeutically- or prophylactically-effective amount of this pharmaceutical composition.

15 In a further aspect, the invention includes a method of producing a polypeptide by culturing a cell that includes a NOVX nucleic acid, under conditions allowing for expression of the NOVX polypeptide encoded by the DNA. If desired, the NOVX polypeptide can then be recovered.

20 In another aspect, the invention includes a method of detecting the presence of a NOVX polypeptide in a sample. In the method, a sample is contacted with a compound that selectively binds to the polypeptide under conditions allowing for formation of a complex between the polypeptide and the compound. The complex is detected, if present, thereby identifying the NOVX polypeptide within the sample.

The invention also includes methods to identify specific cell or tissue types based on their expression of a NOVX.

25 Also included in the invention is a method of detecting the presence of a NOVX nucleic acid molecule in a sample by contacting the sample with a NOVX nucleic acid probe or primer, and detecting whether the nucleic acid probe or primer bound to a NOVX nucleic acid molecule in the sample.

30 In a further aspect, the invention provides a method for modulating the activity of a NOVX polypeptide by contacting a cell sample that includes the NOVX polypeptide with a compound that binds to the NOVX polypeptide in an amount sufficient to modulate the activity of said polypeptide. The compound can be, e.g., a small molecule, such as a nucleic acid, peptide, polypeptide, peptidomimetic, carbohydrate, lipid or other organic (carbon containing) or inorganic molecule, as further described herein.

Also within the scope of the invention is the use of a therapeutic in the manufacture of a medicament for treating or preventing disorders or syndromes including, *e.g.*, Cancer, Leukodystrophies, Breast cancer, Ovarian cancer, Prostate cancer, Uterine cancer, Hodgkin disease, Adenocarcinoma, Adrenoleukodystrophy, Cystitis, incontinence, Von Hippel-Lindau (VHL) syndrome, hypercalceimia, Endometriosis, Hirschsprung's disease, Crohn's Disease, Appendicitis, Cirrhosis, Liver failure, Wolfram Syndrome, Smith-Lemli-Opitz syndrome, Retinitis pigmentosa, Leigh syndrome; Congenital Adrenal Hyperplasia, Xerostomia; tooth decay and other dental problems; Inflammatory bowel disease, Diverticular disease, fertility, Infertility, cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis , atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis , subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, obesity, Diabetes Insipidus and Mellitus with Optic Atrophy and Deafness, Pancreatitis, Metabolic Dysregulation, transplantation recovery, Autoimmune disease, Systemic lupus erythematosus, asthma, arthritis, psoriasis, Emphysema, Scleroderma, allergy, ARDS, Immunodeficiencies, Graft vesus host, Alzheimer's disease, Stroke, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Multiple sclerosis, Ataxiatelangiectasia, Behavioral disorders, Addiction, Anxiety, Pain, Neurodegeneration, Muscular dystrophy, Lesch-Nyhan syndrome, Myasthenia gravis, schizophrenia, and other dopamine-dysfunctional states, levodopa-induced dyskinesias, alcoholism, epileptic seizures and other neurological disorders, mental depression, Cerebellar ataxia, pure; Episodic ataxia, type 2; Hemiplegic migraine, Spinocerebellar ataxia-6, Tuberous sclerosis, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Renal tubular acidosis, IgA nephropathy, and/or other pathologies and disorders of the like.

The therapeutic can be, *e.g.*, a NOVX nucleic acid, a NOVX polypeptide, or a NOVX-specific antibody, or biologically-active derivatives or fragments thereof.

For example, the compositions of the present invention will have efficacy for treatment of patients suffering from the diseases and disorders disclosed above and/or other pathologies and disorders of the like. The polypeptides can be used as immunogens to produce antibodies specific for the invention, and as vaccines. They can also be used to screen for potential agonist and antagonist compounds. For example, a cDNA encoding NOVX may be useful in gene therapy, and NOVX may be useful when administered to a subject in need thereof. By way of non-limiting example, the compositions of the present invention will have efficacy for

treatment of patients suffering from the diseases and disorders disclosed above and/or other pathologies and disorders of the like.

The invention further includes a method for screening for a modulator of disorders or syndromes including, *e.g.*, the diseases and disorders disclosed above and/or other pathologies and disorders of the like. The method includes contacting a test compound with a NOVX polypeptide and determining if the test compound binds to said NOVX polypeptide. Binding of the test compound to the NOVX polypeptide indicates the test compound is a modulator of activity, or of latency or predisposition to the aforementioned disorders or syndromes.

Also within the scope of the invention is a method for screening for a modulator of activity, or of latency or predisposition to disorders or syndromes including, *e.g.*, the diseases and disorders disclosed above and/or other pathologies and disorders of the like by administering a test compound to a test animal at increased risk for the aforementioned disorders or syndromes. The test animal expresses a recombinant polypeptide encoded by a NOVX nucleic acid. Expression or activity of NOVX polypeptide is then measured in the test animal, as is expression or activity of the protein in a control animal which recombinantly-expresses NOVX polypeptide and is not at increased risk for the disorder or syndrome. Next, the expression of NOVX polypeptide in both the test animal and the control animal is compared. A change in the activity of NOVX polypeptide in the test animal relative to the control animal indicates the test compound is a modulator of latency of the disorder or syndrome.

In yet another aspect, the invention includes a method for determining the presence of or predisposition to a disease associated with altered levels of a NOVX polypeptide, a NOVX nucleic acid, or both, in a subject (*e.g.*, a human subject). The method includes measuring the amount of the NOVX polypeptide in a test sample from the subject and comparing the amount of the polypeptide in the test sample to the amount of the NOVX polypeptide present in a control sample. An alteration in the level of the NOVX polypeptide in the test sample as compared to the control sample indicates the presence of or predisposition to a disease in the subject. Preferably, the predisposition includes, *e.g.*, the diseases and disorders disclosed above and/or other pathologies and disorders of the like. Also, the expression levels of the new polypeptides of the invention can be used in a method to screen for various cancers as well as to determine the stage of cancers.

In a further aspect, the invention includes a method of treating or preventing a pathological condition associated with a disorder in a mammal by administering to the subject a NOVX polypeptide, a NOVX nucleic acid, or a NOVX-specific antibody to a subject (*e.g.*, a

human subject), in an amount sufficient to alleviate or prevent the pathological condition. In preferred embodiments, the disorder, includes, e.g., the diseases and disorders disclosed above and/or other pathologies and disorders of the like.

In yet another aspect, the invention can be used in a method to identify the cellular receptors and downstream effectors of the invention by any one of a number of techniques commonly employed in the art. These include but are not limited to the two-hybrid system, affinity purification, co-precipitation with antibodies or other specific-interacting molecules.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides novel nucleotides and polypeptides encoded thereby. Included in the invention are the novel nucleic acid sequences and their encoded polypeptides. The sequences are collectively referred to herein as "NOVX nucleic acids" or "NOVX polynucleotides" and the corresponding encoded polypeptides are referred to as "NOVX polypeptides" or "NOVX proteins." Unless indicated otherwise, "NOVX" is meant to refer to any of the novel sequences disclosed herein. Table A provides a summary of the NOVX nucleic acids and their encoded polypeptides.

TABLE A. Sequences and Corresponding SEQ ID Numbers

NOVX Assignment	Internal Identification	SEQ ID NO (nucleic acid)	SEQ ID NO (polypeptide)	Homology
1a	83420733_EXT	1	2	Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit-like
1b	AL356413.6	3	2	Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit-like

1c	CG52997-02	4	5	Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit-like
2	101599929_EXT1	6	7	Attractin like
3a	124217931_EXT	8	9	Kinase-like
3b	124217931	10	11	RHO/RAC-interacting citron kinase-like
4	105827550_EXT	12	13	Plexin-like
5	GMAC027612_A	14	15	Dopamine receptor-like
6	GM523_e_1_A	16	17	Metabotropic Glutamate Receptor
7a	sggc_draft_ba560a15_20000723_dal	18	19	PV-1-like
7b	2847264.0.32	20	21	PV-1-like
7c	CG51878-03	22	23	PV-1-like
8a	SC134914330_A	24	25	Papin-like
8b	CG57026-04	26	27	Papin-like

NOVX nucleic acids and their encoded polypeptides are useful in a variety of applications and contexts. The various NOVX nucleic acids and polypeptides according to the invention are useful as novel members of the protein families according to the presence of domains and sequence relatedness to previously described proteins. Additionally, NOVX nucleic acids and polypeptides can also be used to identify proteins that are members of the family to which the NOVX polypeptides belong.

NOV1 is homologous to a Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit-like family of proteins. Thus, the NOV1 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example; cancer, cystitis, incontinence, fertility, cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis , atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis , subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, obesity, transplantation recovery, and/or other pathologies/disorders.

NOV2 is homologous to the Attractin-like family of proteins. Thus NOV2 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example; Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Multiple sclerosis, Ataxiatelangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neurodegeneration, Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalceimia, Diabetes, Pancreatitis, Obesity, Endometriosis, Infertility, Hirschsprung's disease, Crohn's Disease, Appendicitis, Muscular dystrophy, Lesch-

Nyhan syndrome, Myasthenia gravis, Cirrhosis, Liver failure, Breast cancer, Ovarian cancer, Prostate cancer, Uterine cancer and/or other pathologies/disorders.

NOV3 is homologous to a family of RHO/RAC-interacting citron kinase-like proteins. Thus, the NOV3 nucleic acids and polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example: asthma, arthritis, psoriasis, diabetes, and IBD, which require activated T cells, as well as diseases such as systemic lupus erythematosus that involve B cell activation, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Renal tubular acidosis, IgA nephropathy, Hypercalceimia, Lesch-Nyhan syndrome, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Endocrine dysfunctions, Obesity, Growth and Reproductive disorders Hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, allergies, immunodeficiencies, transplantation, Lymphaedema, Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host, Hirschsprung's disease, Crohn's Disease, Appendicitis Inflammatory bowel disease, Diverticular disease and/or other pathologies/disorders.

NOV4 is homologous to the Plexin-like family of proteins. Thus, NOV4 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example: Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neurodegeneration, Systemic lupus erythematosus, Autoimmune disease, Asthma, Emphysema, Scleroderma, allergy, ARDS, Obesity, Metabolic Dysregulation, Infertility and/or other pathologies/disorders.

NOV5 is homologous to the Dopamine receptor-like family of proteins. Thus NOV5 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example: schizophrenia, and other dopamine-dysfunctional states, Hypertension, Huntington's disease, levodopa-induced dyskinesias, alcoholism, Diabetes Insipidus and Mellitus with Optic Atrophy and Deafness, Wolfram Syndrome and/or other pathologies/disorders.

NOV6 is homologous to the Metabotropic Glutamate Receptor-like family of proteins. Thus NOV6 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example; epileptic seizures and other neurological disorders, Hodgkin disease, polycystic kidney disease, 5 mental depression, Adenocarcinoma, Smith-Lemli-Opitz syndrome, Retinitis pigmentosa and/or other pathologies/disorders.

NOV7 is homologous to members of the PV-1-like family of proteins. Thus, the NOV7 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example; 10 Cerebellar ataxia, pure; Episodic ataxia, type 2; Hemiplegic migraine, familial; Leigh syndrome; Spinocerebellar ataxia-6; Psoriasis, susceptibility to; Autoimmune disease, Asthma, Emphysema, Scleroderma, allergy, ARDS, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, 15 Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Muscular dystrophy, Myasthenia gravis, Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft vesus host, Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation, Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, 20 Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Scleroderma, Obesity, Transplantation; fertility; cancer; Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalceimia, Lesch-Nyhan syndrome, Adrenoleukodystrophy, Congenital Adrenal Hyperplasia, Xerostomia; tooth decay 25 and other dental problems; Inflammatory bowel disease, Diverticular disease, Pancreatitis, and/or other pathologies/disorders.

NOV8 is homologous to the Papin-like family of proteins. Thus, NOV8 nucleic acids and polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications implicated in, for example; cancer, cystitis, 30 incontinence, fertility, cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, obesity, transplantation recovery and/or other pathologies/disorders.

The NOVX nucleic acids and polypeptides can also be used to screen for molecules, which inhibit or enhance NOVX activity or function. Specifically, the nucleic acids and polypeptides according to the invention may be used as targets for the identification of small molecules that modulate or inhibit, e.g., neurogenesis, cell differentiation, cell proliferation, hematopoiesis, wound healing and angiogenesis.

5 Additional utilities for the NOVX nucleic acids and polypeptides according to the invention are disclosed herein.

NOV1

NOV1 includes three novel Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit (IGFBP-ALS)-like proteins disclosed below. The disclosed sequences have been named NOV1a, NOV1b, and NOV1c. The nucleotide sequences for NOV1a and b both code for the NOV1a protein sequence. The NOV1c nucleic acid sequence codes for the NOV1c protein sequence.

NOV1a

15 A disclosed NOV1a nucleic acid of 2838 nucleotides (also referred to as 83420733_EXT) encoding a novel Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit-like protein is shown in Table 1A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 184-186 and ending with a TAG codon at nucleotides 2707-2709. A putative untranslated region upstream from the initiation codon 20 and downstream from the termination codon is underlined in Table 1A. The start and stop codons are in bold letters.

Table 1A. NOV1a nucleotide sequence (SEQ ID NO:1).

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AACTTTATGAAGCTATGGGACTTGACAAAAAGTGTATTGAGAAGAAAAGTACCGAGTGGGTGGTGTTC
TTTTTTAATAAAGGAATGTGATTACTTGAAACCTCTTCCAGCTGTGCAATTACAGATAACCTCAGGAACAA
GTCTCTGCCTTACAGAAATCGGATTTCATCATGACAACATGAAGCTGTGGATTCACTCTCTTTATTCACTCT
CTCCTTGCGTGTATCTTACACTCCAAACTCCAGTGCTCTCATCCAGAGGCTTGTATTCTCTTCTGCTTCTG
AATGTGAGAAAAAGATGGCAATGCTAATAAATTGTGAAGCAGAAAGGTATCAAGATGGTATCTGAAATA
AGTGTGCCACCATCACGACCTTCCAACAAGCTTAATTAAATAACGGCTTGACCGATGCTTCACACAAATGAC
TTTCTGGCTTACCAATGCTATTCAATACACCTGGATTAAACAATTGCAAGATATTGAGATAGGTGCA
TTAATGGCTTGGCTCTGTGAAACACTCATCAATCAACAAATTCTTAGAAATTCTAAAGAGGAACT
TTCCATGGACTGGAAAACCTGGAAATTCTGCAAGCAGATAAACAAATTTCACAGTGATTGAACCAAGTGCC
TTAGCAACTCAACAGACTCAAAGTGTAAATTAAATGACAATGTATTGAGAGTCTTCCCTCCAACATC
TTCCGATTGTTCTTAAACCCATCTAGATCTTGTGAAATCAATTACAAACATTGCTTATGTTGGTTT
CTCGAACACATTGGCGGAATTGGATCTTCAGTGGAGGACAACAAATGGGCTGCAATTGTACTTATG
CAGTTAAAACATTGGTTGGAGAACATGCCTCCACAGTCATAATTGGATGTGCTCTGCAACAGCCCCCTCCA
TTTTTTAAAGGAAGTAACTCAGTAGACTAAAGAAGGAATCTTGGCTTACTCCACCCAGTGATGAAGAA
CATGAGGATCTTCAGGATCAATTACATGGCAGCAACATCTCAATAAATGATACTCGCATGCAACTAAG
ACCACTGTCATTCTAAACACTACCCACAAAGCACCAGGTTGATACCTTATAATTACAAGCCATCCACTCAA
CTTCCAGGACCTTACTGCCATTCTGTAACTGCAAAGTCTTACCCATCAGGACTTCTAAATACATTGT
CAGGAGCGAACATTGAAGAGCTTACAGATCTGAGACCTCTCCGAAAAATCTAGAAAGCTTACTCTAGG
GGAATATTATTCACAGTTAAATGAGTCTGATCTAGTGGAAATTTCACTTGGAAATGCTTACTTGGGA
AACATCGTATTGAAGTCTTGAAGAAGGATCGTTATGAAACCTAACGAGATTCAAAACTCTATCTAAAT

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GGTAACCACCTGACCAAATTAAAGTAAAGGCATGTTCCCTGGTCTCCATAATCTTGAATACTTATATCTTGAA
TACAATGCCATTAAAGGAATAACTGCCAGGAACCTTTAATCCAATGCCAAAACTTAAAGTCTGTATTTAAAT
AACCAACCTCCTCCAAGTTTACCCACATATTTTCAGGGGTCTCTAACTAAGGTAATCTTAAACAA
AACAGTTACCCATCTACCTGTAAGTAATTTGGATGATCTTGATTACTAACCAGATTGACCTTGAG
GATAACCCCCTGGGACTGCTCCTGTGACCTGGTGGACTCAGCAATGGATACAAAGTAAAGCAAGAACACA
GTGACAGATGACATCCTCTGCACTCCCCGGCATCGACAAAAGGAATTGAAAGCCCTAAATAGTGAA
ATTCTCTGTCAGGTTAGTAATAACCCATCCATGCCAACACAGACTAGTTACCTTATGGTACCAACTCCT
GAACAAACAAACAAATACGGCTGATACTATTTCAGATCTTACGGACGCTGTCCTAATTA
TTGGGACTCTGATTATGTTCATCATTGTTCTGTGCTGCAAGGATAGTGGTTCTTGTCTCACCGC
AGGAGAAAGATAACAAAAGAACAAAGTAGATGACAAATGAGACAAAGTCCTGTGACATCTCAGTAAGC
ATGTATGCCATAAAACCACTCATCACACTGAAAGACCCCTGCTCACTCTATGAAACAGCACATGGTG
AGCCCCATGGTTCATGTCTATAGAAGTCCATCCTTGGTCAAAGCATCTGGAAGAGGAAGAGAGAGGAAT
GAGAAAGAAGGAAGTGTGCAAAACATCTCAAAGAAGTCTTTGGAACAGGAAATCATTACCCACTCAC
GGTCAAATGAAATAACAAACCGAACCAATCAACAGAACTTCTTCAAGATGCCAGCTCATTG
TACAGAAATTTAGAAAAAGGAACCTTCAGCAACTGGGATCACAGAACTTCAAGGAAAAACATT
GCTCAGCTCAGCCTGATATGGAGGCACATTATCTGGAGGCCACAGAGCTGAAGGTTAATGAAACATT
ATGIACTCACGCTCAAGGAAGGTATTAGTGGAACAGACAAAAAAATGAGTATTTGAACTTAAAGCTAATTTA
CATGCTGAACCTGACTATTTAGTCCCTGGAGCAGCAACATAGATGGAGAGTTGAGGGCTTCGCAGAA
ATGCTGTGATTCTGTTAAGTCCATACCTTGAAATTAGTGCCTTACGTGAGTGTCTCATCCATCAGAAC
TAAGCACAGCTAAACTATGGAGAAAAAA

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In a search of public sequence databases, the NOV1a nucleic acid sequence, located on chromosome 13 has 1173 of 1932 bases (61%) identical to a KIAA0848 mRNA from human (gb:GENBANK-ID:AB020655|acc:AB020655). Public nucleotide databases include all 5 GenBank databases and the GeneSeq patent database.

In all BLAST alignments herein, the "E-value" or "Expect" value is a numeric indication of the probability that the aligned sequences could have achieved their similarity to the BLAST query sequence by chance alone, within the database that was searched. For example, the probability that the subject ("Sbjct") retrieved from the NOV1 BLAST analysis, 10 e.g., thioredoxin mRNA from *Ovis aries*, matched the Query NOV1 sequence purely by chance is 7.4e⁻⁶⁸. The Expect value (E) is a parameter that describes the number of hits one can "expect" to see just by chance when searching a database of a particular size. It decreases exponentially with the Score (S) that is assigned to a match between two sequences. Essentially, the E value describes the random background noise that exists for matches 15 between sequences.

The Expect value is used as a convenient way to create a significance threshold for reporting results. The default value used for blasting is typically set to 0.0001. In BLAST 2.0, the Expect value is also used instead of the P value (probability) to report the significance of matches. For example, an E value of one assigned to a hit can be interpreted as meaning that 20 in a database of the current size one might expect to see one match with a similar score simply by chance. An E value of zero means that one would not expect to see any matches with a similar score simply by chance. See, e.g., <http://www.ncbi.nlm.nih.gov/Education/BLASTinfo/>. Occasionally, a string of X's or N's will result from a BLAST search. This is a result of automatic filtering of the query for low-

complexity sequence that is performed to prevent artifactual hits. The filter substitutes any low-complexity sequence that it finds with the letter "N" in nucleotide sequence (e.g., "NNNNNNNNNNNNNN") or the letter "X" in protein sequences (e.g., "XXXXXX"). Low-complexity regions can result in high scores that reflect compositional bias rather than significant position-by-position alignment. (Wootton and Federhen, Methods Enzymol 266:554-571, 1996).

The disclosed NOV1a polypeptide (SEQ ID NO:2) encoded by SEQ ID NO:1 has 841 amino acid residues and is presented in Table 1B using the one-letter amino acid code. Signal P, Psort and/or Hydropathy results predict that NOV1a has a signal peptide and is likely to be localized in the plasma membrane with a certainty of 0.4600. In other embodiments, NOV1a may also be localized to the endoplasmic reticulum (membrane) with a certainty of 0.1000, the endoplasmic reticulum (membrane) with a certainty of 0.1000, or extracellularly with a certainty of 0.1000. The most likely cleavage site for a NOV1a peptide is between amino acids 20 and 21, at: LHS-QT.

SNP data for NOV1a can be found below in Example 3. SAGE data can also be found below for NOV1a in Example 4.

Table 1B. Encoded NOV1a protein sequence (SEQ ID NO:2).

MKLWIHILFYSSLLACISLHSQTPVLSSRGSCDSLNCCEKDGTMLINCEAKGIKMVSEISVPPS RPFQLSLLNNNGLTMILHTNDFSGLTNAISIHLGFNNIADIEIGAFNGLGLLKQLHINHNSLEILK EDTFHGLENLFLQADNNFITVIEPSAFSKLNRLKVLILNDNAIESLPNIFRFVPLTHLDLRG NQLQTLPYVGFLFHIGRILDLQLEDNKWACNCDDLLQLKTWLLENMPPOSIIGDVVCNSPFFKGS TLSRLKESICPTPPVYEEHEDPSGSLSHLAATSSINDSRMSTKTTTSILKLPDKAPGLIPYITKP STQLPGPYCPICPCNCKVLSLSPSGLILHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLV EYFTLEMLHLGNNRIEVLEEGSFMLTRLQKLYLNGNHLTKLSKGMLGLHNLEYLYEYNAIK EILPGTFNPMPKLVLYLNNNLLQVLPPHIFSGVPLTKVNLTQFTHLPVSNILDLDLLTQI DLEDNPWDCCSDLVGLQQWIQKLISKNTVTIDILCTSPGHLDDKKELKALNSEILCPGLVNNFSMP TQTSYLMVTTPATTTNTADTTILRSLTDAPVLSVLTILGLLIMFITIVFCAGIVVVLVILHRRRYK KKQVDEQMRDNSPVHLQYSMYGHKTTHHTTERPSASLYEQHMVSPMVHVYRSPSFGPKHLEEEE ERNEKEGSDAKHLQRSLLEQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYRNILEKERELQO LGITEYLRKNIAQLQPDMEARHPGAHEELKLMETLMSRPRKVVLVEQTNEYFELKANLHAEPD YLEVLEQQT
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A search of sequence databases reveals that the NOV1a amino acid sequence has 266 of 543 amino acid residues (49%) identical to, and 337 of 543 amino acid residues (62%) similar to the 977 amino acid residue KIAA0848 protein from human (SPTREMBL-ACC:O94933) ($E = 1.6e^{-165}$), and 350 of 841 amino acid residues (41%) identical to, and 511 of 841 amino acid residues (60%) similar to the 845 amino acid residue Human gene 1

encoded secreted protein HMIAJ30 (patp:AAE01232) ($E = 1.6e^{-156}$). Public amino acid databases include the GenBank databases, SwissProt, PDB and PIR.

NOV1a is expressed in at least the following tissues: breast, heart, bladder, colon, prostate, brain, lung and uterus. TaqMan expression data for NOV1a is shown below in

5 Example 2.

NOV1b

A disclosed NOV1b nucleic acid of 2526 nucleotides (also referred to as AL356413.6) encoding a novel Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit-like protein is shown in Table 1C. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TAG codon at nucleotides 2524-2526. A putative untranslated region upstream from the initiation codon is underlined in Table 1C. The start and stop codons are in bold letters.

Table 1C. NOV1b nucleotide sequence (SEQ ID NO:3).

<pre> ATGAAGCTGTGGATTCATCTTTTATTCACTCTCCTTGCTGTATATCTTTACACTCCCAAAC TCCAGTGCTCTCATCCAGAGGCTTGTGATTCTTTGCAATTGTGAGGAAAAGATGGCACAA TGCTAATAAATTGTGAAAGCAAAAGGTATCAAGATGGTATCTGAAATAAGTGTGCCACCATCACGA CCTTTCCAACTAAGCTTATTAAATAACGGCTTGACGATGCTTCACACAAATGACTTTCTGGGCT TACCAATGCTATTTCATAACACCTTGATTAAACAATATTGAGATATTGAGATAGGTGCATTAA ATGGCCTGGCCTCTGAAACAACTTCATATCAATCACAATTCTTAGAAATTCTAAAGAGGAT ACTTTCCATGGACTGGAAAACCTGGAATTCTGCAAGCAGATAACAATTATCACACTGATTGA ACCAAGTGCCTTAGCAAGCTCAACAGACTCAAAAGTGTAAATTAAATGACAATGCTATTGAGA GTCTTCTCCAAACATCTTCCGATTGTCCTTAAACCCATCTAGATCTCGTGGAAATCAATTAA CAAACATTCGCTTATGTTGGTTTCTCGAACACATGGGCGAATATTGAGATCTCAGTTGGAGGA CAACAAATGGGCTGCAATTGTGACTTATTGAGTTAAACATGGTTGGAGAACATGCCCTCAC AGTCTATAATTGGTGTGTTGCTGCAACAGCCTTCATTTTAAAGGAAGTATACTCAGTAGA CTAAAGAAGGAATCTATTGCCCCACTCCACCCAGTGTATGAAGAACATGAGGATCCTCAGGATC ATTACATCTGGCAGCAACATCTCAATAATGATAGTCGCATGTCAACTAAGACCACGTCCATT TAAAACCTACCCACCAAAGCACCAGGTTGATACCTTATATTACAAAGCCATCCACTCAACTCCA GGACCTTACTGCCCTATTCTTGTAACTGCAAAGTCCCTATCCCCTCAGGACTTCTAATACATTG TCAGGAGCGCAACATTGAAAGCTTATCAGATCTGAGACCTCCTCCGAAAATCTAGAAAGCTCA TTCTAGGGAAATATTATTCACAGTTAAATGAAAGTCTGATCTAGTGGAAATATTCACTTTGGAA ATGCTTCACTGGGAAACAATCGTATTGAAAGTCTGAGAAGGATCGTTTATGAACCTAACGAG ATTACAAAAAACTCTATCTAAATGTTGAAACACCTGACCAAAATTAAGTAAAGGCATGTTCTGGTC ATTCATAATCTGAAACTTATCTGAAATCAATGCCATTAAAGGAATTAACGACTTACCTGACAGCTT AATCCAATGCCCTAAACATTAAAGTCTGATTAAATAACACCTCCTCCAAGTTTACCCACACA TATTTTTCAGGGGTCTCTCAACTAAGGTAATCTTAAACAAACCAAGTTTACCCATCTACCTG TAAGTAAATTGGATGATCTGATTGCTAACCCAGATGACCTTGAGGATAACCCCTGGGAC TGCTCCTGTGACCTGGTGGACTGCAGCAATGGATACAAAGTTAAGCAAGAACACAGTGACAGA TGACATCCTCTGCACTTCCCCCGGCATCTGACAAAAAGGAATTGAAAGCCCTAAATAGTAAA TTCTCTGTCAGGTTAGTAAATAACCCATCCATGCCAACACAGACTAGTTACCTTATGGTCACC ACTCCCTGCAACAACAACAAATAACGGCTGATACTATTTCAGATCTCTACGGACGGCTGTGCCACT GTCTGTTCTAATATTGGGACTTCTGATTATGTCATCACTATTGTTTCTGTGCTGAGGGATAG TGGTTCTGTTCTCACCGCAGGAGAAGATAACAAAAGAACAGTAAAGTGGCAAAATGAGAGAC AACAGTCCCTGTGCATCTCAGTACAGCATGTATGGCCATAAAACCACTCATCACACTGAAAG ACCCCTGCCCCACTCTATGAACAGCACATGGTGGAGCCCCATGGTTCATGTCATAGAAGTCCAT CCTTTGGCCAAAGCATCTGGAAGAGGAAGAGAGGAATGAGAAGAAGAGGAAGTGTGCAAAAC CATCTCCAAGAAGTCTTTGGAACAGGAAAATCATTCACTCACAGGGTCAAATATGAAATA </pre>
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CAAAACCACGAACCAATCAACAGAATTTCATCCTTCCAAGATGCCAGCTCATGGTACAGAAACA  
TTTAGAAAAAGAAGGGAACCTTCAGCAACTGGGAATCACAGAATACCTAACGGAAAACATTGCT  
CAGCTCCAGCCTGATATGGAGGCACATTATCTGGAGCCACGAAGAGCTGAAGTTAATGGAAAC  
ATTAATGTACTCACGTCCAAGGAAGGTATTAGTGGAACAGACAAAAATGAAGTATTITGAACCTTA  
AAGCTAATTACATGCTGAACCTGACTATTAGAAGTCCTGGAGCGACAAACATAG
```

The disclosed NOV1b nucleotide encodes the NOV1a protein sequence disclosed above in Table 1B.

5 **NOV1c**

In the present invention, the target sequence identified previously, NOV1b, was subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. In each case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such primers were designed based on *in silico* predictions for the full length cDNA, part (one or more exons) of the DNA or protein sequence of the target sequence, or by translated homology of the predicted exons to closely related human sequences or sequences from other species. These primers were then employed in PCR amplification based on the following pool of human cDNAs: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain - whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea, uterus. Usually the resulting amplicons were gel purified, cloned and sequenced to high redundancy. The resulting sequences from all clones were assembled with themselves, with other fragments in CuraGen Corporation's database and with public ESTs. Fragments and ESTs were included as components for an assembly when the extent of their identity with another component of the assembly was at least 95% over 50 bp. In addition, sequence traces were evaluated manually and edited for corrections if appropriate. These procedures provide the sequence reported below, which is designated NOV1c (also referred to as Accession Number CG52997-02). This is a mature protein with 100% identity to the previously identified sequence NOV1b.

30 A disclosed NOV1c nucleic acid of 2531 nucleotides (also referred to as CG52997-02) encoding a novel Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit-like protein is shown in Table 1D. An open reading frame was identified beginning with a

GAT initiation codon at nucleotides 2-4 and ending with a TAA codon at nucleotides 2513-2515. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 1D. The start and stop codons are in bold letters. Because the start codon is not a traditional ATG start codon, the reading frame shown below for NOV1c could be a partial reading frame that extends further in the 5' direction.

Table 1D. NOV1c nucleotide sequence (SEQ ID NO:4).

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GGATTCTCTTTTATTCACTCTCCTGCCTGTATATCTTACACTCCCAAACCTCCAGTGCTCTCATCCAG
AGGCTCTGTGATTCTCTTGCATTGTGAGGAAAAAAGATGCCAACATGCTAATAAAATTGTGAAGCAAAGG
TATCAAGATGGTATCTGAAATAAGTGTGCTACCACATCACGACCTTCCAACTAAGCTTATTAATAACGGCTT
GACCATGCTTCACACAAATGACTTTCTGGGCTTACCAATGCTTATTCAAATACACCTTGGATTAAACAATAT
TGCGAGATTGAGATAGGTGCATTATGGCCTTGCCTGAAACAACITCATATCAATCACAAATTCCTT
AGAAAATTCTTAAAGAGGAGATACTTCCATGGAACTGGAACTTCTGCAAGCAGATAACAATTITAT
CACAGTGAATTGACCAAGTGCCTTACAGCTAACAGACTCAAAGTGTAAATTAAATGACAATGCTAT
TGAGAGTCTCTCCAAACATCTCCGATTGTTCTTAAACCATCTAGATCTCGTGGAAATCAATTACA
AACATTGCCATTGTTGGTTCTCGAACACATTGGCGGAATTGGATCTTCAGTTGGAGGAAACAAATG
GGCCCTGCAATTGTGACTTATTGCGATTAAAATCTGGGAGAACATGCCCTCACAGTCTATAATTGGTGA
TGTTGTCGAAACAGCCCCTACATTAAAGGAAGTATACTCAGTAGACTAAAGAGGAATCTATTGCCC
TACTCCACCTGATGAAAGAACATGAGGATCTTCAGGATCATTACATCTGGCAGCAACATCTCAATAAA
TGATAGTCGATGTCACAACTAACGACCACTGCCATTCTAAACACTACCCACCAAAAGCACCAGGTTGATACCTTA
TATTACAAAGCCATCCACTCAACTTCCAGGACCTACTGCCCTATTCTGTACTGCAAAGTCTATCCCC
ATCAGGACTTCTAAATACATTGTCAGGAGCGAACATTGAAAGCTTACAGATCTGAGACCTCCCGAAAAA
TCCTAGAAAAGCTTACCTAGCGGGAAATATTACAGCTTAAAGTGAAGTCTGATCTAGTGGAAATATTGAC
TTTGGAAATGCTTCACTGGGAAACAAATCGTATTGAAAGTCTGAAAGGATCGTTATGAAACCTAACGAG
ATTACAAAATCTATCTAAATGGTAACCACTGCCAAATTAAAGTAAAGGATGTTCTGGTCTCCATAA
TCTGAAATACTTATATCTGAAATACAATGCCATTAGGAATACTGCCAGGAACCTTAAATCCAATGCC
ACTTAAAGTCTGTATTAAATAACACCTCCCAAGTTTACGCCACATAATTTCAGGGGTTCTCT
AACTAAGGTAATCTTAAACAAACAGTACCTTACCCATCTACCTGTAAGTAAATTTGGATGATCTGATTT
GCTAACCCAGATTGACCTTGAGGATAACCCCTGGGACTGCTCTGACCTGGACTGCGACATGGAT
ACAAAAGTTAACGCAAGAACACAGTGAACAGATGACATCTGCACTTCCCCGGCATCTGACAAAAAGGA
ATTGAAAGGCCCTAAATAGTGAATTCTCTGTCAGGTTAGTAAATAACCCATCATGCCAACACAGACTAG
TTACCTTATGGTACCACTCTGCAACAAACAACAAATACGGCTGATACTATTACGATCTCTACGGACCC
TGTCGCACTGCTGTTCAATTGGACTCTGATTATGTTCTCATCACTATTGTTCTGTCCTGCAAGGGAT
AGTGGTTCTGTTCTCACCGCAGGAGAACATACAAAAGAACAACTAGATGAGCAATGAGAGAACACAG
TCTCTGCACTTCACTGCACTGATGTTCAATTAAACCACTCATCACTACTGAAAGACCCCTGCTC
ACTCTATGACAGCACATGGTGAGCCCCATGGTTCACTGCTATAGAAGTCCATCTGGTCAAAGCATCT
GGAAGAGGAAGAGAGAGGAATGAGAAAAGAAGGAAGTGATGCAAAACATCTCCAAAGAAGTCTTGGAA
GAAAATCATTCAACCTCACAGGTCAAATGAAATAACAAAACACGAAACCAATCAAAGAATTCTTATC
CTTCCAAGATGCCAGCTCATGTCAGAAACATTGTTAGAAAAAGAACACTCAGCAACTGGGAATCAC
AGAATACCTAAAGGAAAACATTGTCAGCTCCAGCTGTATGGAGGACATTAATCTGGAGCCCAGAAGA
GCTGAAGTTAATGGAAACATTAATGTACTCACGTCAGGAAAGGTATTAGTGGAAACAGACAAAAAATGAGT
TTTGAACCTAAAGCTAATTACATGCTGAACCTGACTATTAGAAGTCTGGAGCAGCAAACATAAGGGCG
AATTCTGCTG

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In a search of public sequence databases, the NOV1c nucleic acid sequence, located on chromosome 13 has 2471 of 2480 bases (99%) identical to a gb:GENBANK-

10 ID:AK026427|acc:AK026427.1 mRNA from *Homo sapiens* (*Homo sapiens* cDNA: FLJ22774
fis, clone KAIA1575) (E = 0.0). Public nucleotide databases include all GenBank databases and the GeneSeq patent database.

The disclosed NOV1c polypeptide (SEQ ID NO:5) encoded by SEQ ID NO:4 has 837 amino acid residues and is presented in Table 1E using the one-letter amino acid code. Signal 15 P, Psort and/or Hydropathy results predict that NOV1c has no signal peptide and is likely to be

localized in the plasma membrane with a certainty of 0.4600. In other embodiments, NOV1c may also be localized to the endoplasmic reticulum (membrane) with a certainty of 0.1000, the endoplasmic reticulum (membrane) with a certainty of 0.1000, or extracellularly with a certainty of 0.1000.

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Table 1E. Encoded NOV1c protein sequence (SEQ ID NO:5).

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DSLFYSSLLACISLHSQTPVLSSRGSCDSLNCCEEKDGTMILINCEAKGIKMVSEISVLPSPRFQLSLLNNGL
TMLHTNDFSGLTNAISIHLGFNNIADIEIGAFNGLGLLKOLHINNSLEILKEDTFHGLENLFLQADNNFI
TVIEPSAFSKLNRLKVLILNDNAIESLPPNIFPRFVPLTHLDLRGNQLQTLPYVGFLEHIGRILDLQLEDNKW
ACNCDDLLKTWLENMPQSIIGDVVCNSPPFFKGSIISRLRKESICPTPPVYEEHEDPSGSLSLHAATSSIN
DSRMSTKTTISILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSLPSGLLIHQCERNIESLSSDLRPPPQN
PRKLILAGNIIHSLMKSDLVEYFTLMLHLCGNNRIVELEEGSFMLNTRIQKLYLNGNHLTKLISKGMFLGLHN
LELYILEYNAITKEILPCTFPNPMPKLKVLYLNNNNLQVLPPHIFSGVPLTKVNLTQFTHLPVSNILDDDL
LTQIDLEDNPWDSCDVLQQWIQLSKNTVTDDILCTSPGHLDKALNSELCPGLVNPNPSMPTQTS
YLMVTTPAATTNTADTTLRSLTDAVPLSVLILGLIMFITIVFCAGIVVVLVLERRRRYKKRQVDEQMRDNS
PVHLQYSMYGHKTTHTTERPSASLYEQHMVSPMVHVYRSPSFGPKHLEEEEERNEKEGSDAKHLQRSLLEQ
ENHSPLTGNSNMKYKTTNQSTEFLSFQDASSLYRNILEKERELQQLGITTEYLKNTIAQLQPDMEAHYPGAHEE
LKLMEETLMSRPRKVLIQEQTKEYLHAEPDYLEVLEQQT

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A search of public sequence databases reveals that the NOV1c amino acid sequence has 427 of 436 amino acid residues (97%) identical to, and 428 of 436 amino acid residues (98%) similar to, the 440 amino acid residue ptnr:SPTRREMBL-ACC:Q9H5Y7 protein from 10 *Homo sapiens* (Human) (CDNA: FLJ22774 FIS, CLONE KAIA1575) ($E = 5.7e^{-230}$). Public amino acid databases include the GenBank databases, SwissProt, PDB and PIR.

NOV1c is expressed in at least the following tissues: Heart, Coronary Artery, Pancreas, Small Intestine, Peripheral Blood, Brain, Mammary gland/Breast, Uterus, Vulva, Prostate, Lung, Trachea, Skin, Colon. Expression information was derived from the tissue sources of 15 the sequences that were included in the derivation of the sequence of NOV1c.

The proteins encoded by the NOV1a, 1b and 1c nucleotides are very closely homologous as is shown in the alignment in Table 1F. As shown, the sequences encoded by the NOV1a and 1b nucleic acid sequences are 100% identical.

Table 1F Alignment of NOV1a, 1b, and 1c.

	10	20	30	40	50	60	
NOV1a	
NOV1b	MKLWIHLFYSSLLACISLHSQTPVLSSRGSCDSLNCCEEKDGTMILINCEAKGIKMVSEIS						
NOV1c	MKLWIHLFYSSLLACISLHSQTPVLSSRGSCDSLNCCEEKDGTMILINCEAKGIKMVSEIS						
	-----DSLFYSSLLACISLHSQTPVLSSRGSCDSLNCCEEKDGTMILINCEAKGIKMVSEIS						
	70	80	90	100	110	120	
NOV1a	VPPSRPFQLSLLNNGLTMLHTNDFSGLTNAISIHLGFNNIADIEIGAFNGLGLLKOLHIN						
NOV1b	VPPSRPFQLSLLNNGLTMLHTNDFSGLTNAISIHLGFNNIADIEIGAFNGLGLLKOLHIN						
NOV1c	VPPSRPFQLSLLNNGLTMLHTNDFSGLTNAISIHLGFNNIADIEIGAFNGLGLLKOLHIN						
	130	140	150	160	170	180	
NOV1a	
NOV1b	HNSLEILKEDTFHGLENLFLQADNNFIVIEPSAFSKLNRLKVLILNDNAIESLPPNIF						

	NOV1c	HNSLEILKEDTFHGLENLLEFLQADNNFITVIEPSAFSKLNRLKVILNDNATESLPPNIF
		190 200 210 220 230 240
5	NOV1a	RFVPLTHLDLRCGNQLQTLFVYGVFLEHIGRILDLOLEDNKWACNC DLLQLKTWLENMPPQS
	NOV1b	RFVPLTHLDLRCGNQLQTLFVYGVFLEHIGRILDLOLEDNKWACNC DLLQLKTWLENMPPQS
	NOV1c	RFVPLTHLDLRCGNQLQTLFVYGVFLEHIGRILDLOLEDNKWACNC DLLQLKTWLENMPPQS
10		250 260 270 280 290 300
	NOV1a	IIGDVVCNSPPFKGSILSRLKKECICPTPPVYEEHEDPSGSLHLAAATSSINDSRMSTKT
	NOV1b	IIGDVVCNSPPFKGSILSRLKKECICPTPPVYEEHEDPSGSLHLAAATSSINDSRMSTKT
	NOV1c	IIGDVVCNSPPFKGSILSRLKKECICPTPPVYEEHEDPSGSLHLAAATSSINDSRMSTKT
15		310 320 330 340 350 360
	NOV1a	TSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCVKVLSPSGLLIHQCERNIESLSDLRP
	NOV1b	TSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCVKVLSPSGLLIHQCERNIESLSDLRP
	NOV1c	TSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCVKVLSPSGLLIHQCERNIESLSDLRP
20		370 380 390 400 410 420
	NOV1a	PPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNRRIEVELEEGSFMNLTQLQKLYLNG
	NOV1b	PPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNRRIEVELEEGSFMNLTQLQKLYLNG
25	NOV1c	PPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNRRIEVELEEGSFMNLTQLQKLYLNG
		430 440 450 460 470 480
30	NOV1a	NHLTLSKGFMGLHLNLEYLYLEYNAIKEILPGTFNPMPKLVLYLNNNNLQVLPPIIFS
	NOV1b	NHLTLSKGFMGLHLNLEYLYLEYNAIKEILPGTFNPMPKLVLYLNNNNLQVLPPIIFS
	NOV1c	NHLTLSKGFMGLHLNLEYLYLEYNAIKEILPGTFNPMPKLVLYLNNNNLQVLPPIIFS
35		490 500 510 520 530 540
	NOV1a	GVPLTKVNLTQNFTHLPVSNIIDDDLLTQIDLEDNPWDCSCDLVGLQQWIQKLSKNTV
	NOV1b	GVPLTKVNLTQNFTHLPVSNIIDDDLLTQIDLEDNPWDCSCDLVGLQQWIQKLSKNTV
	NOV1c	GVPLTKVNLTQNFTHLPVSNIIDDDLLTQIDLEDNPWDCSCDLVGLQQWIQKLSKNTV
40		550 560 570 580 590 600
	NOV1a	TDDILCTS PGHLDKKELKALNSEILCPGLVNNPSMPTQTSYLMVTTPATTTNTADTILRS
	NOV1b	TDDILCTS PGHLDKKELKALNSEILCPGLVNNPSMPTQTSYLMVTTPATTTNTADTILRS
	NOV1c	TDDILCTS PGHLDKKELKALNSEILCPGLVNNPSMPTQTSYLMVTTPATTTNTADTILRS
45		610 620 630 640 650 660
	NOV1a	LTD AVPLS VLILGLLIMFITIVFCAGIVVVLVLRHRRRYKKKQVDEQMRD NSP VHL QYSM
	NOV1b	LTD AVPLS VLILGLLIMFITIVFCAGIVVVLVLRHRRRYKKKQVDEQMRD NSP VHL QYSM
	NOV1c	LTD AVPLS VLILGLLIMFITIVFCAGIVVVLVLRHRRRYKKKQVDEQMRD NSP VHL QYSM
50		670 680 690 700 710 720
	NOV1a	YGHKTTHHTTERPSASLYE QHMVSPMVHVYRSPSF GPKHLEEEEERNEKEGSDAKH LQRS
	NOV1b	YGHKTTHHTTERPSASLYE QHMVSPMVHVYRSPSF GPKHLEEEEERNEKEGSDAKH LQRS
	NOV1c	YGHKTTHHTTERPSASLYE QHMVSPMVHVYRSPSF GPKHLEEEEERNEKEGSDAKH LQRS
55		730 740 750 760 770 780
	NOV1a	LLEQENHSPLTGSNMKYKTTTNQSTEPLSFQDASSLYRNILEKERELQQLGITEYL RKNIA
	NOV1b	LLEQENHSPLTGSNMKYKTTTNQSTEPLSFQDASSLYRNILEKERELQQLGITEYL RKNIA
	NOV1c	LLEQENHSPLTGSNMKYKTTTNQSTEPLSFQDASSLYRNILEKERELQQLGITEYL RKNIA
60		790 800 810 820 830 840
	NOV1a	QLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQT KNEYFELKANLHAEPDYLEVLEQQ
	NOV1b	QLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQT KNEYFELKANLHAEPDYLEVLEQQ
	NOV1c	QLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQT KNEYFELKANLHAEPDYLEVLEQQ

NOV1a T (SEQ ID NO:2)
 NOV1b T (SEQ ID NO:2)
 NOV1c T (SEQ ID NO:5)

5 Homologies to any of the above NOV1 proteins will be shared by the other two NOV1 proteins insofar as they are homologous to each other as shown above. Any reference to NOV1 is assumed to refer to all three of the NOV1 proteins in general, unless otherwise noted.

The disclosed NOV1a polypeptide has homology to the amino acid sequences shown in the BLASTP data listed in Table 1G.

10

Table 1G. BLAST results for NOV1a					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Po sitives (%)	Expect
gi 14758126 ref XP_033182.1	hypothetical protein FLJ22774 [Homo sapiens]	798	798/798 (100%)	798/798 (100%)	0.0
gi 14149932 ref NP_115605.1	hypothetical protein FLJ22774 [Homo sapiens]	440	425/425 (100%)	425/425 (100%)	0.0
gi 6691962 emb CAB65788.1	bG256O22.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit)) [Homo sapiens]	853	354/866 (40%)	504/866 (57%)	e-161
gi 11360190 pir T46279	hypothetical protein DKFZp564O1278.1 - human (fragment)	314	314/314 (100%)	314/314 (100%)	e-160
gi 14424224 sp 094991 Y918 HUMAN	HYPOTHETICAL PROTEIN KIAA0918	966	356/915 (38%)	534/915 (57%)	e-158

15 The homology between these and other sequences is shown graphically in the ClustalW analysis shown in Table 1H. In the ClustalW alignment of the NOV1 protein, as well as all other ClustalW analyses herein, the black outlined amino acid residues indicate regions of conserved sequence (*i.e.*, regions that may be required to preserve structural or functional properties), whereas non-highlighted amino acid residues are less conserved and can potentially be altered to a much broader extent without altering protein structure or function.

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Table 1H. ClustalW Analysis of NOV1

- 1) Novel NOV1a (SEQ ID NO:2)
- 2) Novel NOV1b (SEQ ID NO:2) (Identical to NOV1a)
- 3) Novel NOV1c (SEQ ID NO:5)

- 4) gi|14758126|ref|XP_033182.1| hypothetical protein FLJ22774 [Homo sapiens] (SEQ ID NO:28)
 5) gi|14149932|ref|NP_115605.1| hypothetical protein FLJ22774 [Homo sapiens] (SEQ ID NO:29)
 5) 6) gi|6691962|emb|CAB65788.1| bG256022.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit)) [Homo sapiens] (SEQ ID NO:30)
 7) gi|11360190|pir||T46279 hypothetical protein DKFZp564O1278.1 - human (fragment (SEQ ID NO:31)
 8) gi|14424224|sp|094991|Y918_HUMAN HYPOTHETICAL PROTEIN KIAA0918 (SEQ ID NO:32)

10

	10	20	30	40	50
NOV1a
NOV1b	MKLWIHLFYSSLACISLHSQTPV
NOV1c	MKLWIHLFYSSLACISLHSQTPV
gi 14758126	DSLFYSSLACISLHSQTPV
gi 14149932
gi 6691962	YFSLFRSIQLFADCK-KMFLWLFLILS	AQISSTNADSD
gi 11360190
gi 14424224	RRGAQGGKMHTCPPVTLEQDLHRKMHSWMLQTL	AFAVTS	VLSCAETID

15

	60	70	80	90	100
NOV1a	SSRGSCSICNCCEEKDGIML	LINCEAKGIKMKVSEISVPPSRPFQLSILNNNG
NOV1b	SSRGSCSICNCCEEKDGIML	LINCEAKGIKMKVSEISVPPSRPFQLSILNNNG
NOV1c	SSRGSCSICNCCEEKDGIML	LINCEAKGIKMKVSEISVPPSRPFQLSILNNNG
gi 14758126	MLINCEAKGIKMKVSEISVPPSRPFQLSILNNNG
gi 14149932	MLINCEAKGIKMKVSEISVPPSRPFQLSILNNNG
gi 6691962	ISVEIQN-VCSQSVSENVVYV	NCEKVSVYRPNQIKPPWSNFYHLNFQNNF
gi 11360190	YYGETCDNAACPCEEKDGITVSCENRGITISYSETSPRFPTVHLIISGNL
gi 14424224

20

	110	120	130	140	150
NOV1a	LTMLHTNDFSGLTNAISIHLGFNNIADIEIGAFNGLGLLKQLHINHNSLE
NOV1b	LTMLHTNDFSGLTNAISIHLGFNNIADIEIGAFNGLGLLKQLHINHNSLE
NOV1c	LTMLHTNDFSGLTNAISIHLGFNNIADIEIGAFNGLGLLKQLHINHNSLE
gi 14758126	LTMLHTNDFSGLTNAISIHLGFNNIADIEIGAFNGLGLLKQLHINHNSLE
gi 14149932	LTMLHTNDFSGLTNAISIHLGFNNIADIEIGAFNGLGLLKQLHINHNSLE
gi 6691962	LNQIYENTFLNFSHAVSHIHLGNNNKLNQIEEGAFLGLSALKQLHLNNNEIK
gi 11360190	LNRLIPENEFVNNTGASIIHLGSNVHQDIEIGAFHGLRGLRFLHNNNKE
gi 14424224

25

	160	170	180	190	200
NOV1a	ILKEDTFHGLENLLEFLQADNNFITVIEPSAFSKLNRLKVLILNDNAIESL
NOV1b	ILKEDTFHGLENLLEFLQADNNFITVIEPSAFSKLNRLKVLILNDNAIESL
NOV1c	ILKEDTFHGLENLLEFLQADNNFITVIEPSAFSKLNRLKVLILNDNAIESL
gi 14758126	ILKEDTFHGLENLLEFLQADNNFITVIEPSAFSKLNRLKVLILNDNAIESL
gi 14149932	ILKEDTFHGLENLLEFLQADNNFITVIEPSAFSKLNRLKVLILNDNAIESL
gi 6691962	ILRADIFLGTEENLEYLQADYNYLKYIERGAPNKLHKLKVLLNDNLSL
gi 11360190	ILRADIFLGTEENLEYLQADYNYLKYIERGAPNKLHKLKVLLNDNLSL
gi 14424224	ILRADIFLGTEENLEYLQADYNYLKYIERGAPNKLHKLKVLLNDNLSL

40

	210	220	230	240	250
NOV1a	PPNIIFRFVPLTHLDLRGNQLQTLPYVGFLFHIGRILDLQLEDNKWCACNCD
NOV1b	PPNIIFRFVPLTHLDLRGNQLQTLPYVGFLFHIGRILDLQLEDNKWCACNCD
NOV1c	PPNIIFRFVPLTHLDLRGNQLQTLPYVGFLFHIGRILDLQLEDNKWCACNCD
gi 14758126	PPNIIFRFVPLTHLDLRGNQLQTLPYVGFLFHIGRILDLQLEDNKWCACNCD
gi 14149932	PPNIIFRFVPLTHLDLRGNQLQTLPYVGFLFHIGRILDLQLEDNKWCACNCD
gi 6691962	PPNIIFRFVPLTHLDLRGNQLQTLPYVGFLFHIGRILDLQLEDNKWCACNCD
gi 11360190	PPNIIFRFVPLTHLDLRGNQLQTLPYVGFLFHIGRILDLQLEDNKWCACNCD
gi 14424224	PPNIIFRFVPLTHLDLRGNQLQTLPYVGFLFHIGRILDLQLEDNKWCACNCD

55

	260	270	280	290	300
NOV1a	LLQLKTIWLENMPQSIIIGDVVCNSPPFFKGSILSRLKKESTCPTPPVYRE
NOV1b	LLQLKTIWLENMPQSIIIGDVVCNSPPFFKGSILSRLKKESTCPTPPVYRE

	NOV1c	LLQLKTIWLENMPQSIIGDVVCNSPFFKGSTIISRIKKKESTCPTPPVYEE
5	gi 14758126	LLQLKTIWLENMPQSIIGDVVCNSPFFKGSTIISRIKKKESTCPTPPVYEE
	gi 14149932	LLQLKTIWLENMPQSIIGDVVCNSPFFKGSTIISRIKKKESTCPTPPVYEE
	gi 6691962	LLPLKAWLENNEPYNIYIGEATCETPSDLYGRILKETNKQELCEMGTSDF
	gi 11360190	LIESLKDWLDSTSISYALVGDVVCETEFLHGRDUDDEVSKOELCEMGTSDF
	gi 14424224	LIESLKDWLDSTSISYALVGDVVCETEFLHGRDUDDEVSKOELCEMGTSDF
		310 320 330 340 350
10	NOV1a	HED--PSGSLEHLAATSSINDSRMSKCTSHIKLPLTKAPG-----
	NOV1b	HED--PSGSLEHLAATSSINDSRMSKCTSHIKLPLTKAPG-----
	NOV1c	HED--PSGSLEHLAATSSINDSRMSKCTSHIKLPLTKAPG-----
	gi 14758126	HED--PSGSLEHLAATSSINDSRMSKCTSHIKLPLTKAPG-----
	gi 14149932	DVR-TLEPSOLENGYTIPNCH--TTOTSLRILVTKPKK-TTNP SK-----
	gi 6691962	EMRPQTPLSITGYLHTTPASVNSVAISSSAVYKPLKPKGTRQPNKPRV
	gi 11360190	-----
	gi 14424224	-----
		360 370 380 390 400
20	NOV1a	-----LIPVTTIKPSTOOLPGPYCIPCNCKVLS-PSGLIIE-----
	NOV1b	-----LIPVTTIKPSTOOLPGPYCIPCNCKVLS-PSGLIIE-----
	NOV1c	-----LIPVTTIKPSTOOLPGPYCIPCNCKVLS-PSGLIIE-----
	gi 14758126	-----LIPVTTIKPSTOOLPGPYCIPCNCKVLS-PSGLIIE-----
	gi 14149932	-ISGIVAGKALSNRNLSQLSYQTRVPELTCPACPCFCKTHPSDLGLSYN
	gi 6691962	-----
	gi 11360190	-----
	gi 14424224	RPTSRQPSKDLGYSNYGESPAYOKSPVPLECFTACSCNQISDLGLSYN
		410 420 430 440 450
30	NOV1a	-----
	NOV1b	-----
	NOV1c	-----
	gi 14758126	CQERNIESSESDLRPPONERPKLILACNIIIHSIMKSDLVEYFTILEMLHLCN
	gi 14149932	CQERNIESSESDLRPPONERPKLILACNIIIHSIMKSDLVEYFTILEMLHLCN
	gi 6691962	CQERNIESSESDLRPPONERPKLILACNIIIHSIMKSDLVEYFTILEMLHLCN
	gi 11360190	CQERNIESSESDLRPPONERPKLILACNIIIHSIMKSDLVEYFTILEMLHLCN
	gi 14424224	CQERNIESSESDLRPPONERPKLILACNIIIHSIMKSDLVEYFTILEMLHLCN
		460 470 480 490 500
40	NOV1a	-----
	NOV1b	-----
	NOV1c	-----
	gi 14758126	NRIEVILEEGSFPMNLTRLQKLYLNGNHEITKLSKGMLGLHNLEYLYLE YMA
	gi 14149932	NRIEVILEEGSFPMNLTRLQKLYLNGNHEITKLSKGMLGLHNLEYLYLE YMA
	gi 6691962	NRIEVILEEGSFPMNLTRLQKLYLNGNHEITKLSKGMLGLHNLEYLYLE YMA
	gi 11360190	NRIEVILEEGSFPMNLTRLQKLYLNGNHEITKLSKGMLGLHNLEYLYLE YMA
	gi 14424224	NRIEVILEEGSFPMNLTRLQKLYLNGNHEITKLSKGMLGLHNLEYLYLE YMA
		510 520 530 540 550
50	NOV1a	-----
	NOV1b	-----
	NOV1c	-----
	gi 14758126	IKEILPGETNPMPKLIKLYLNNNLLQVLPPPFI FSGPPLTKVNLKINGETH
	gi 14149932	IKEILPGETNPMPKLIKLYLNNNLLQVLPPPFI FSGPPLTKVNLKINGETH
	gi 6691962	IKEILPGETNPMPKLIKLYLNNNLLQVLPPPFI FSGPPLTKVNLKINGETH
	gi 11360190	IKEISAGTFDSMENLOTLYLNNNLLKSLPVYIFSGAPIARLNLRNKXKMY
	gi 14424224	IREIQSGTFDPVPLNLOLFLNNNLLQAMPSCVFSGPPLTKVNLKINGETH
		560 570 580 590 600
60	NOV1a	-----
	NOV1b	-----
	NOV1c	-----
	gi 14758126	LPVSNTLLEDDLDLTQIDLEDNPWDSCCDLVGLQQWIKLSKNTVTDDILC
	gi 14149932	LPVSNTLLEDDLDLTQIDLEDNPWDSCCDLVGLQQWIKLSKNTVTDDILC
	gi 6691962	LPVSNTLLEDDLDLTQIDLEDNPWDSCCDLVGLQQWIKLSKNTVTDDILC
	gi 11360190	-----LKTWEENMPQ8IICDWWC
	gi 14424224	LPVSCVLELOLQSLTQIDLEGNPWDCTCDLVALKLNWEKLSDGIVVKELK C
		610 620 630 640 650
65	NOV1a	-----
	NOV1b	-----
	NOV1c	-----
	gi 14758126	LPVSNTLLEDDLDLTQIDLEDNPWDSCCDLVGLQQWIKLSKNTVTDDILC
	gi 14149932	LPVSNTLLEDDLDLTQIDLEDNPWDSCCDLVGLQQWIKLSKNTVTDDILC
	gi 6691962	LPVSNTLLEDDLDLTQIDLEDNPWDSCCDLVGLQQWIKLSKNTVTDDILC
		660 670 680 690 700
70	NOV1a	-----
	NOV1b	-----
	NOV1c	-----
	gi 14758126	LPVSNTLLEDDLDLTQIDLEDNPWDSCCDLVGLQQWIKLSKNTVTDDILC
	gi 14149932	LPVSNTLLEDDLDLTQIDLEDNPWDSCCDLVGLQQWIKLSKNTVTDDILC
	gi 6691962	LPVSNTLLEDDLDLTQIDLEGNPWDCTCDLVALKLNWEKLSDGIVVKELK C

gi 11360190LOQNIQKLSKNTVTDDILC
gi 14424224	LPVSGYLDQQLKSLEQIDLHDNPWDCNCDIVGMKLWVEOLKVGVIVDDEVIC
	610 620 630 640 650
5 NOV1a	TSPGHLDKKELKALNSEIILCPG--LVNNPSMPTQI--SYLMVTTPATT
NOV1b	TSPGHLDKKELKALNSEIILCPG--LVNNPSMPTQI--SYLMVTTPATT
NOV1c	TSPGHLDKKELKALNSEIILCPG--LVNNPSMPTQI--SYLMVTTPATT
10 gi 14758126	TSPGHLDKKELKALNSEIILCPG--LVNNPSMPTQI--SYLMVTTPATT
gi 14149932	NSPPFFKGSLSRKEKESICE--TTPVYEEHE--DPGSGLHLAAT
gi 6691962	EAPVQFANEIELKSLEKNEILCP--KLNKPS--APFTSPAPAIT
gi 11360190	TSPGHLDKKELKALNSEIILCPG--LVNNPSMPTQI--SYLMVTTPATT
gi 14424224	KAPKKFAETDMRSIKSELCLFDYSDVVNSTPTPSSTIQVPAARTSAVTPAVR
	660 670 680 690 700
15 NOV1a	TNTADTILRSLTDAT--PLSVLILGLLIMFITIVFCAGIVVLVLHRR
NOV1b	TNTADTILRSLTDAT--PLSVLILGLLIMFITIVFCAGIVVLVLHRR
NOV1c	TNTADTILRSLTDAT--PLSVLILGLLIMFITIVFCAGIVVLVLHRR
20 gi 14758126	TNTADTILRSLTDAT--PLSVLILGLLIMFITIVFCAGIVVLVLHRR
gi 14149932	ESINDSRMSMKITTS--I--I--KPTKAAPGLIP--
gi 6691962	FTTPPLGPFRSPPGG--PVPLSILILSLIVLVLILIVFVAFCLLIVFVLRRN
gi 11360190	TNTADTILRSLTDAT--PLSVLILGLLIMFITIVFCAGIVVLVLHRR
gi 14424224	LNSTGAPASLGAGGGASSVPLSVLILSLLVFIMSVFVAAGLIVLVMKRR
	710 720 730 740 750
25 NOV1a	RRYKKKQVDQEQRDNDSPVHLQYSMYG--HKTTHTTERPSAS--
NOV1b	RRYKKKQVDQEQRDNDSPVHLQYSMYG--HKTTHTTERPSAS--
NOV1c	RRYKKKQVDQEQRDNDSPVHLQYSMYG--HKTTHTTERPSAS--
30 gi 14758126	RRYKKKQVDQEQRDNDSPVHLQYSMYG--HKTTHTTERPSAS--
gi 14149932	--YTTKPSQOLPGPYCPIIPCNCKYLSP--SGLLIHQCERNIES
gi 6691962	KKPTVKHEGLGNPDCGSMQLOU--RKHDKINKKDGLS--
gi 11360190	RRYKKKQVDQEQRDNDSPVHLQYSMYG--HKTTHTTERPSAS--
35 gi 14424224	KKNQSDHTSTNNSDVSSEMOYSIVYEGGGTGGPHAHVHHRCPALPKVK
	760 770 780 790 800
40 NOV1a	LYEQHMVSPMVHVYRSPSFGPKHLE--EEEERNEKEG--
NOV1b	LYEQHMVSPMVHVYRSPSFGPKHLE--EEEERNEKEG--
NOV1c	LYEQHMVSPMVHVYRSPSFGPKHLE--EEEERNEKEG--
gi 14758126	LYEQHMVSPMVHVYRSPSFGPKHLE--EEEERNEKEG--
gi 14149932	--LSD--I--RPPPQNPRKLI--LAGNIIHS--
gi 6691962	--TEAFIPOQHGEOMSHKSHCGLKES--ETGFMFSE--
45 gi 11360190	LYEQHMVSPMVHVYRSPSFGPKHLE--EEEERNEKEG--
gi 14424224	TPAGHVYVLYLPEDLGHCMKFLYRSREGNSVEDYKDLHELKVTYSSNHL
	810 820 830 840 850
50 NOV1a	SDAK--HLQRSLLEQENHSPLTGSNMKY--KTTINQST
NOV1b	SDAK--HLQRSLLEQENHSPLTGSNMKY--KTTINQST
NOV1c	SDAK--HLQRSLLEQENHSPLTGSNMKY--KTTINQST
gi 14758126	SDAK--HLQRSLLEQENHSPLTGSNMKY--KTTINQST
gi 14149932	--LMKSDLVEVETLEMHLIGNNRI--EVLEFG--
55 gi 6691962	--PPGC--KVMVRNVADEKDLHVDTTRKR-LSTIPELD
gi 11360190	SDAK--HLQRSLLEQENHSPLTGSNMKY--KTTINQST
gi 14424224	QQQQQPPPPPQQQQQQPPQPOLOLQPGEEERRESHHLRSPAVSVTIEPRE
	860 870 880 890 900
60 NOV1a	EFL-SFQDASSLYRNILEKERELQQLGITEYLRK--NIA-QLQPD
NOV1b	EFL-SFQDASSLYRNILEKERELQQLGITEYLRK--NIA-QLQPD
NOV1c	EFL-SFQDASSLYRNILEKERELQQLGITEYLRK--NIA-QLQPD
gi 14758126	EFL-SFQDASSLYRNILEKERELQQLGITEYLRK--NIA-QLQPD
gi 14149932	--SEMNLTRLOKLYLNCG--HLTKDSKGMLFLG--LHN
gi 6691962	ELF-PSRDTSNVTIONFLESXKEYNSIGVSG--
gi 11360190	EFL-SFQDASSLYRNILEKERELQQLGITEYLRK--NIA-QLQPD
gi 14424224	DLLSPVQDADREYRGILEPDKHCSTTPAGNSLPEYPKFPCSPAAYTFSPN
	910 920 930 940 950

	
	NOV1a	MEAHYPGAH-----EELKLMETLMSRPRKVVLVEQTKEFYFELKANLHAE
	NOV1b	MEAHYPGAH-----EELKLMETLMSRPRKVVLVEQTKEFYFELKANLHAE
	NOV1c	MEAHYPGAH-----EELKLMETLMSRPRKVVLVEQTKEFYFELKANLHAE
5	gi 14758126	MEAHYPGAH-----EELKLMETLMSRPRKVVLVEQTKEFYFELKANLHAE
	gi 14149932	LEVILYLEYN-----AIKETIIPGTFNPMP-----KLKVLYLNMTSSKFYHIIFFQ
	gi 6691962	FETRYPEK-----QP-----DKKSCKSEIIGGNHSKIVVEQRNSYEFELKANLQSS
	gi 11360190	MEAHYPGAH-----EELKLMETLMSRPRKVVLVEQTKEFYFELKANLHAE
	gi 14424224	YDLRRPHQYLHPGAGHSRLREPVLYSPPSAVEVEPNRNEYLELKAKLNVE
10		960
	
	NOV1a	PDYLEVLEQQT-----
	NOV1b	PDYLEVLEQQT-----
	NOV1c	PDYLEVLEQQT-----
15	gi 14758126	PDYLEVLEQQT-----
	gi 14149932	G-----
	gi 6691962	PDYLVLEEQTALNKI
	gi 11360190	PDYLEVLEQQT-----
20	gi 14424224	PDYLEVLEKQQTTPSQF

The presence of identifiable domains in NOV1, as well as all other NOVX proteins, was determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website (<http://www.ebi.ac.uk/interpro>). DOMAIN results for NOV1 as disclosed in Tables 1I-1L, were collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections. For Table 1E and all successive DOMAIN sequence alignments, fully conserved single residues are indicated by black shading or by the sign () and “strong” semi-conserved residues are indicated by grey shading or by the sign (+). The “strong” group of conserved amino acid residues may be any one of the following groups of amino acids: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW.

Tables 1I-1L lists the domain description from DOMAIN analysis results against NOV1. This indicates that the NOV1 sequence has properties similar to those of other proteins known to contain this domain.

Table 11. Domain Analysis of NOV1

gnl|Smart|smart00082, LRRCT, Leucine rich repeat C-terminal domain.
(SEQ ID NO:65)
CD-Length = 51 residues, 100.0% aligned
Score = 49.7 bits (117), Expect = 7e-07

Table 1J. Domain Analysis of NOV1

gnl|Smart|smart00082, LRRCT, Leucine rich repeat C-terminal domain.
 (SEQ ID NO:65)
 CD-Length = 51 residues, 100.0% aligned
 Score = 45.1 bits (105), Expect = 2e-05

5 Query: 218 NKWACNC DLLQLK TWL ENMPPQ SIIGDV VCNS PPF KGS ILS RLK KES ICP 268
 | + | + | + | | | + | + | | | + | + | | | |
 Sbjct: 1 NPFICDC ELRW LLR WL QAN RHL QDP VDL RCAS PESL RGPL LLL PSS FKC P 51

Table 1K. Domain Analysis of NOV1

gnl|Pfam|pfam01463, LRRCT, Leucine rich repeat C-terminal domain.
 Leucine Rich Repeats pfam00560 are short sequence motifs present in a number of proteins with diverse functions and cellular locations. Leucine Rich Repeats are often flanked by cysteine rich domains. This domain is often found at the C-terminus of tandem leucine rich repeats (SEQ ID NO:66)
 CD-Length = 51 residues, 100.0% aligned
 Score = 47.8 bits (112), Expect = 3e-06

10 Query: 517 NPWDCSC DLV GLQQ WIQ KLS KNT VTDDI LCT SP GHLD KKEL KALN SE IL CP 567
 || + | | + | | + | ++ + | + | | | | + | | + | |
 Sbjct: 1 NPFICDC ELRW LLR WL REPR RL ED PED LR CAS PESL RGPL LLL P SDF FSCP 51

Table 1L. Domain Analysis of NOV1

gnl|Pfam|pfam01463, LRRCT, Leucine rich repeat C-terminal domain.
 Leucine Rich Repeats pfam00560 are short sequence motifs present in a number of proteins with diverse functions and cellular locations. Leucine Rich Repeats are often flanked by cysteine rich domains. This domain is often found at the C-terminus of tandem leucine rich repeats. (SEQ ID NO:66)
 CD-Length = 51 residues, 100.0% aligned
 Score = 46.2 bits (108), Expect = 7e-06

15 Query: 218 NKWACNC DLLQLK TWL ENMPPQ SIIGDV VCNS PPF KGS ILS RLK KES ICP 268
 | + | + | + | | | + | + | | | + | + | | |
 Sbjct: 1 NPFICDC ELRW LLR WL REPR RL ED PED LR CAS PESL RGPL LLL P SDF FSCP 51

20 Proteins belonging to the IGFBP-ALS family of proteins play an important role in regulating the levels of circulating hormones. The acid labile subunit of the complex plays an important role in regulating the stability of the complex and ensuring high levels of circulating hormones that are regulated by the IGFBP family of proteins. This protein also has a leucine rich repeat that is a common domain in many proteins that are important for the developing embryo. As a result this protein may play an important role in development and disease.

Insulin-like growth factors (IGFs) I and II are important regulators of cell proliferation and differentiation (Ueki I et al., Proc Natl Acad Sci U S A 2000 Jun 6;97(12):6868-73). After birth, plasma IGFs, representing mostly liver-derived IGFs, circulate in ternary complexes of 150 kDa consisting of one molecule each of IGF, IGF-binding protein (IGFBP) 3, and an acid labile subunit (ALS). Onset of ALS synthesis after birth is the primary factor driving the formation of ternary complexes. Capture of IGFs by ALS is thought to allow the development of a plasma reservoir without negative effects such as hypoglycemia and cell proliferation. To evaluate the importance of ALS and ternary complexes, we have created mice in which the ALS gene has been inactivated. The mutation was inherited in a Mendelian manner, without any effects on survival rates and birth weights. A growth deficit was observed in null mice after 3 weeks of life and reached 13% by 10 weeks. This modest phenotype was observed despite reductions of 62 and 88% in the concentrations of plasma IGF-I and IGFBP-3, respectively. Increased turnover accounted for these reductions because indices of synthesis in liver and kidney were not decreased. Surprisingly, absence of ALS did not affect glucose and insulin homeostasis. Therefore, ALS is required for postnatal accumulation of IGF-I and IGFBP-3 but, consistent with findings supporting a predominant role for locally produced IGF-I, is not critical for growth. This model should be useful to determine whether presence of ALS is needed for other actions of liver-derived IGF-I and for maintenance of homeostasis in presence of high circulating levels of IGF-II.

In circulation, insulin-like growth factor-I (IGF-I) is bound in a trimeric complex of 150 kDa with IGF binding protein-3 (IGFBP-3) and the acid-labile subunit (ALS). (Moller S et al., J Hepatol 2000 Mar;32(3):441-6). Whereas circulating IGF-I and IGFBP-3 are reported to be low in patients with chronic liver failure, the level of ALS has not been described in relation to hepatic dysfunction. The aim of the present study was therefore to measure circulating and hepatic venous concentrations of ALS in relation to hepatic function and the IGF axis.

The insulin-like growth factor (IGF) binding proteins (IGFBPs) were initially identified as carrier proteins for IGF-I and IGF-II in a variety of biologic fluids. (Rosenfeld RG et al., Pediatrics 1999 Oct;104(4 Pt 2):1018-21). Their presumed function was to protect IGF peptides from degradation and clearance, increase the half-life of the IGFs, and deliver them to appropriate tissue receptors. The concept of IGFBPs as simple carrier proteins has been complicated, however, by a number of observations: 1) the six IGFBPs vary in their tissue expression and their regulation by other hormones and growth factors; 2) the IGFBPs are subjected to proteolytic degradation, thereby altering their affinities for the IGFs; 3)

IGFBP-3 and IGFBP-5, in addition to binding IGFs, also can associate with an acid-labile subunit, thereby increasing further the half-life of the IGFs; 4) in addition to modifying the access of IGF peptides to IGF and insulin receptors, several of the IGFBPs may be capable of increasing IGF action; 5) some of the IGFBPs may be capable of IGF-independent regulation of cell growth; 6) some of the IGFBPs are associated with cell membranes or possibly with membrane receptors; and 7) some of the IGFBPs have nuclear recognition sites and may be found within the nucleus. Additionally, a number of cDNAs identified recently have been found to encode proteins that bind IGFs, but with substantially lower affinities than is the case with IGFBPs. The N-terminal regions of the predicted proteins are structurally homologous to the classic IGFBPs, with conservation of the cysteine-rich region. These observations suggest that these low-affinity binders are members of an IGFBP superfamily, capable of regulating cell growth by both IGF-dependent and IGF-independent mechanisms.

Total IGF-I level in serum is a sensitive index during growth hormone (GH) replacement therapy of adults, since GH stimulates the hepatic expressions of both insulin-like growth factor (IGF-I) and acid-labile subunit (ALS) and the major part of IGF-I in the circulation is found in a ternary complex together with ALS and IGFBP-3. (Hall K et al., J Endocrinol Invest 1999;22(5 Suppl):48-57) However, other regulators of the proteins constituting the ternary complex may influence IGF-I levels. In healthy subjects the serum IGF-I levels are low at birth, rise during childhood, with peak levels during puberty, and decline with increasing age. This pattern has been attributed to the age-dependent GH production, but it is unknown whether the wide range of IGF-I levels within each age interval is due to GH production or GH sensitivity. In elderly twins approximately 60% of IGF-I levels are genetically determined. The remaining environmental dependency of IGF-I is partly due to nutrition. Both caloric and protein content of the diet is of importance. Thus, low IGF-I levels are found in GH deficient patients as well as in patients with GH resistance due to malnutrition or GH receptor defects. It is essential that IGF-I determination is performed by assays in which IGFBPs do not interfere, and that IGF-I concentration is evaluated in relation to age, i.e. expressed in SD score, and the number of individuals constituting the reference intervals improves the sensitivity and specificity. Although determination of IGF-I is recommended in assessing GH deficiency in children, its diagnostic value in patients with adult onset of GH deficiency is not agreed upon. In the age group above 40-80 years many patients with pituitary/hypothalamic disorders and GH peaks below 3 µg/l during provocation tests have normal IGF-I levels. It is not clarified, whether the IGF-I levels within normal range for age is

due to endogenous basal GH production being sufficient or other factors stimulating IGF-I, IGFBP-3 or ALS expressions.

Circulating insulin-like growth factors (IGFs) represent an important pool of potential hypoglycemic activity, which is largely inhibited by their sequestration in a heterotrimeric complex comprising growth factor, IGF-binding protein-3 (IGFBP-3), and acid-labile subunit (ALS). (Baxter RC Metabolism 1995 Oct;44(10 Suppl 4):12-7). Less than 1% of total IGFs circulate in the free form, yet even this amount might contribute significantly to circulating insulin-like activity. The ternary binding protein complex appears to inhibit insulin-like activity of bound IGFs by preventing their egress from the circulation. Although the integrity of this complex might be affected by limited proteolysis of IGFBP-3 in pregnancy and catabolic conditions, the evidence that this increases IGF bioavailability, and thus hypoglycemic potential, is as yet unclear. However, in patients with IGF-II-secreting tumors, hypoglycemia may result from a failure of the ternary complex to adequately sequester the IGFs. Improvement in complex formation, by treatment with corticosteroids or growth hormone, alleviates the hypoglycemia, even if (as seen with growth hormone treatment) IGF-II hypersecretion persists. In these patients, blood glucose levels are inversely correlated with IGFBP-2 levels, suggesting that this protein might play a part in transporting IGFs to their target tissues. Conversely, ALS levels correlate positively with blood glucose, emphasizing the importance of the ternary complex in preventing hypoglycemia. Unlike the other IGF-binding proteins, IGFBP-1 is acutely regulated in the circulation, in a manner consistent with its acting as a glucose counterregulator. It might act in this way by inhibiting the activity of free IGFs in the circulation.

Leucine-rich repeats (LRRs) are relatively short motifs (22-28 residues in length) found in a variety of cytoplasmic, membrane and extracellular proteins (InterPro). Although these proteins are associated with widely different functions, a common property involves protein-protein interaction. Little is known about the 3D structure of LRRs, although it is believed that they can form amphipathic structures with hydrophobic surfaces capable of interacting with membranes. In vitro studies of a synthetic LRR from Drosophila Toll protein have indicated that the peptides form gels by adopting beta-sheet structures that form extended filaments. These results are consistent with the idea that LRRs mediate protein-protein interactions and cellular adhesion. Other functions of LRR-containing proteins include, for example, binding to enzymes and vascular repair. The 3D structure of ribonuclease inhibitor, a protein containing 15 LRRs, has been determined, revealing LRRs to be a new class of

alpha/beta fold. LRRs form elongated non-globular structures and are often flanked by cysteine rich domains.

The disclosed NOV1 nucleic acid of the invention encoding a Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit -like protein includes the nucleic acid 5 whose sequence is provided in Table 1A, C and E or a fragment thereof. The invention also includes a mutant or variant nucleic acid any of whose bases may be changed from the corresponding base shown in Table 1A, C, or E while still encoding a protein that maintains its Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit-like activities and physiological functions, or a fragment of such a nucleic acid. The invention further includes 10 nucleic acids whose sequences are complementary to those just described, including nucleic acid fragments that are complementary to any of the nucleic acids just described. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications. Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones 15 are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject. In the mutant or variant nucleic acids, and their complements, up to about 10% percent of the bases may be so changed.

20 The disclosed NOV1 protein of the invention includes the Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit-like protein whose sequence is provided in Table 1B or 1E. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in Table 1B or 1E while still encoding 25 a protein that maintains its Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit -like activities and physiological functions, or a functional fragment thereof. In the mutant or variant protein, up to about 60% percent of the residues may be so changed.

The invention further encompasses antibodies and antibody fragments, such as F_{ab} or (F_{ab})₂, that bind immunospecifically to any of the proteins of the invention.

30 The above defined information for this invention suggests that this Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit-like protein (NOV1) may function as a member of a "Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit family". Therefore, the NOV1 nucleic acids and proteins identified here may be useful in potential therapeutic applications implicated in (but not limited to) various pathologies and disorders as indicated below. The potential therapeutic applications for this invention include,

but are not limited to: protein therapeutic, small molecule drug target, antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), diagnostic and/or prognostic marker, gene therapy (gene delivery/gene ablation), research tools, tissue regeneration *in vivo* and *in vitro* of all tissues and cell types composing (but not limited to) those defined here.

5 The NOV1 nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in cancer including but not limited to various pathologies and disorders as indicated below. For example, a cDNA encoding the Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit-like protein (NOV1) may be useful in gene therapy, and the Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit -like protein (NOV1) may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from cancer, cystitis, incontinence, fertility, cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis , atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary 10 stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, obesity, transplantation recovery. The NOV1 nucleic acid encoding the Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

15 NOV1 nucleic acids and polypeptides are further useful in the generation of antibodies that bind immuno-specifically to the novel NOV1 substances for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-NOVX Antibodies" section below. The disclosed NOV1 protein has multiple hydrophilic regions, each of which 20 can be used as an immunogen. In one embodiment, a contemplated NOV1 epitope is from about amino acids 10 to 50. In another embodiment, a NOV1 epitope is from about amino acids 80 to 120. In additional embodiments, NOV1 epitopes are from about amino acids 180 to 220, from about amino acids 230 to 300, from about amino acid 330 to 350, from about amino acid 370 to 400, from about amino acid 480 to 540, from about amino acid 550 to 560, 25 and from about amino acids 620 to 840. These novel proteins can be used in assay systems for functional analysis of various human disorders, which will help in understanding of pathology of the disease and development of new drug targets for various disorders.

NOV2

A disclosed NOV2 nucleic acid of 3609 nucleotides (also referred to as 101599929_EXT1) encoding a novel Attractin like protein is shown in Table 2A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 7-9 and 5 ending with a TAA codon at nucleotides 3562-3564. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 2A, and the start and stop codons are in bold letters.

Table 2A. NOV2 nucleotide sequence (SEQ ID NO:6).

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CACTGGATGCAGAAGGCAGACAGCAGCACCGAGACAGCATGAAGGGAGAAGAGGACACGGGCTGCCATACCGTG
CGGCACAGGACCGGCTCTGCTTCTCGGGCCGCTGTGTCACACTCCACCTGCCCTCGGACCCGGCTGGGTC
GGGACCACTGCCAGCAGCTGCCAGGGCAGGTTAACAGAACCTCTGGTATTAAACAGATGGCCCA
ATTAACTATAAATATAAAACTAAATGACTTGGCTCATTTGAAAGGCCAACATGCAAGTTAACAGATGGCCCA
AATCATTGGCTACAGAATGTAGCTGGATCATATGTTATGATGGAGATTCATATATGCAACCTTA
ATAGCTCTTTAGTGGTTGATAGTCCCTGAATAAGGGCAATGAAACTGTGCTCTGAAGTTGTTACTACA
TCTGGTATGCACTGTACATTTTAGTGTGCTGCGTATAATCTAACAGTGGTTCAACATTTCTATTG
ATCAATTCTGCTCTAACAAATTGCTCTGGTATGGAAAGTGTACAACTAGTGTCTCTGTTCCAAGTCAAGTA
TATTGTAATGTGATAAAATACTGGAAAGGGTAAAGGCTTGATGATATTCTTACIGTAAGCCAAATTGCGGCAGT
CCAGATCAGGTTACTGTGACCTGACTGGAGAAAATTATGTCGTCATGATGTTGGCAAGGTATAGGT
CTGATTGTTCTTGAATGTTCCCTACTGAGCTTACTGGATTCTGCCAAACGTTAACCCCTCAGTCT
TCTGTAGGTGGGCTTACATAAAGCAGTTTACAGGGAAATTATGTTGGGATTTGGGATATACTTTT
AACTACAGTTCTTCAATGGCTCTAACATTAGAAAGCAGTATATGGAATGTAGGAACCTCCATCA
AGGGACCTCTCCAGAGATATGGACACTCTCTGCTTATATCAGGAAACATCTTTATGTTGGAGGAGA
ATTGAAACAAATGATGGAATGTCAAGATGAAATTATGGGTTTAAACATACATAGTCAGTCATGGAGTACA
AAAATCCTACTGTTCTGGACATGGTCAAGTATGCTGTGAGGACATTCAACATATTATGGAGTTG
GATAGTAGAGATGTTGTCATGATCAATAATTGGATATTCTGCAATATATGGTTATAAGCAGCATACAG
GAATACCATACTGTCAAACACTTGGCTTGTCCAGAAACTAAAGGAGCTATTGACAAGGGGATATGGC
CATACTAGTGTGATGAAATAACAAAGTCCATTATGTTCATGGAGGGTATAAGCATTGGCAGGGAAC
AAATATGGATTGGTTGATGTTATAAAATGAGTTAACACTAAAGACTTGGACTATTGGAAAGGAAAGT
GGGTTGGCAGATACCTCATTCACTGGTCTTATCAATGGAGCTATGCTTATTGGAGGAAATACCCAT
AAAGACACTTCTGAGTAACGGTGAACGGTGAACATGGTCTTCTGCCGATTTCTGGCATATGACATGCCAGGC
TGGAGTGCAGTGGCAGCATCTCAGCTACTGCCACCTCCACCTCCAGTCAAGCATTCTCAATAGGTCC
ATGTTATATTGGGGATTTCAGTGTACTCTTAATGATATCTTGTATACAGCCTCAAATTGCAAG
GTTTCAGAGATGAAAGACTTTGTAAGGCTGCTGAGGATGGGAAATGGGAAAGGAAACTCTGAGT
GAATCTTGGGAAACTCTGGGAAACTAAATGAGGAAATGGGAAAGGAGCTGAGTCAATTGGGGATGCT
TGTCTTAGTCAATTCCAGTAGAGGAAACTATGAGGAAATGGGAAACTCTTGTGAGTCAATTGGGAAAT
CTTGGCTTCATTAACACCTCAAAGAAGTAGAATTGTTCTGGATGAAATACAGAAGTATAACACAGAAA
GTATCACCTTGGGATGGCTTGCAGAAGATCAATATCTTATTGGGATGGGAAACATGTCCTTACA
AACACAAACTACAGTGGCTTCTGGCAACCCAAATGATTCTGGTTTGTGCAATCTGGAAAGGGCTGCA
GTGGCAGGCTTAAAGGTAATCTTGTACATCTATGGCAATGGGCTTGTCTGTAACCTTGGGAAACCTGTTAATCAA
AATGCGAGGGCGTGCACAAAGGCAATGCTCTGTGAGGACATCATGTCACCTGGCAACTGACAAGCAATGGGAGTGGAG
TGTATGTGGCAGCAGTACGGAAAGCAAGTGTGTCATCTAATGCTTATATGCTTCTTCCATATGGGAA
TGTCTAGTGGCAAACCTGCCACCTGCTCCCTGCTCAAATTGTTCTGGATGAGAACCTGTCAGTGT
TTGGAAACGCTGTAATGGCTGGTCAATGATCTTAGTAATACAGGAAGAGGACATTGCAATTGCAAGGTTCT
TCACGGGGACCAATGAACTTATTGGAAATGCAACCAAGTGAGGATGGTCTTGTGACCCAAATCTTGGCCCAA
GAAAAGAACTATGAGTGGCTCTTATCCAGTGTCCAGCTGGCACTGTAATGGACATAGCATTGCAAT
ATAATGTCGGAACACGTGAAACACTTAAACAAACTTAAATCTCAACACAGGAGCTGCAAGATGTTATGCAAGGTTATTAT
GGAGATCCACCAATGGGGACAGTGCACAGCTGTACATGCAAGTGGCCATGCAAAATATCTGTCATCTGCAC
ACAGGAAATGTTCTGCAACACTAAAGGAATAAAAGGTGACCAATGCCAAATTGTTGACTCTGAAATCGC
TATGTTGGTAATCACTTAGAGGAACATGTTATTGTAATGAGCTTGTGATTATCAATTACCTTC
AGCTTATTACAGGAAGATGATGCCACCATCTGCCATAAAACTTATGCAACCCAGAACAGGTGAGGAAA
AATCTGGATATCAATTAAATGCAACACACTTAACTCAACACAGGAGCTGCAAGATGTTATGCAAGGTTATTAT
ACAATATCTGGGGAAAGAGACTTCTATAGTTCTCAAGAATAATATAAGGAATACAGAGATGTTCTTCTAT
GAAAATTAACCTTAAAGCAATCTAACATTACATTCTATGTCAGTCAGCAACTTCTGGCCTTAT
AAAATACAGGTAAGTGTAAAGAGTATTCTAATGACCATAATCTTAAAGAAAAGAATGGTGTCTT
GTCCAAAGT

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The disclosed NOV2 nucleic acid sequence, localized to chromosome 10, has 494 of 694 bases (71%) identical to an Attractin protein mRNA from mouse (GENBANK-ID: AF119821) ($E = 2.9e^{-204}$).

5 A NOV2 polypeptide (SEQ ID NO:7) encoded by SEQ ID NO:6 has 1185 amino acid residues and is presented using the one-letter code in Table 2B. Signal P, Psort and/or Hydropathy results predict that NOV2 does not contain a signal peptide and is likely to be localized in the mitochondrial membrane space with a certainty of 0.3600. In other embodiments, NOV2 may also be localized to the microbody (peroxisome) with a certainty of 10 0.3000, or the lysosome (lumen) with a certainty of 0.1000.

Table 2B. Encoded NOV2 protein sequence (SEQ ID NO:7).

MQKADSSTETMKEKRTAAAITVRHRTGSCFGRCVNSTCLCDPGWVGDQCQHCQGRFRRLTEPSGYLTDGPIN YKYKTKCTWLIEGPNAVLRLRFNHATECSWDHMVVDGDSIYAPLIAFSGLIVPEIRGNETVPVVTTSG YALLHHFSDAAYNLTGFNFNIFYSINSPCPNCSGHGKCTSVSPSQVYCECDKYWKGEACDIPYCKANCGSPD HGYCDLTGEKLCVCNDSWQGIGPDCSILNPVSTESYWILPNVKPFSPSVGRASHKAVLHGKFMWVIGGYTFNY SSFPQMVLSSYLNLESSIWNVGTPSRGPLQRYGHSLALYQENIFMYGRIETNDGNVTDELWVFNIHSQSWSTKT PTVVLGHGQOQYAVECHSAHIMELSDRVMMIIIFGYSAIYGYTSSIQYEYHICNTWLVPETKGAIIVQGGYGH SVYDEITKSIVVHGGYKALPGNKYGLVDDLYKYEVNTKTWTILKESGFARYLHSAVINGAMLIPGGNTHND TSLSNGAKFCFSADFLAYDICPGWSAVERSQLTATSTSHVQALINRSMYIFGGFSSVLLNDILVYKEPNCKAF RDEELCKNAGPGIKCVWNKNHCESWESGNTNNILRAKCFSKRNLCSDRCYRADCASCTANTNGCQWCDDKK CISANSNCMSVISFGYITLPSQFPFYCYRYADCASCTANTNGCQWCDDKKCIALPAHLCGEGWSHIGDACL RVNNSRENVYDNAKLYCVNLSGNLASLTTSKVEVFVLDIJKYTQOKVSPVGLRKINISYWGWEDEMSPTFTNT TLQWLPGEPNDSGFCAYLERAAVAGLKNPCTSMANGLVCEKPVNQARPCKKPCSLRTSCSNCTSNGMECM WCSSTKRCVDSNAYIISPYGQCLEWQATCSRAQNCGLRTCGOCLEQPECGWCDPNTGRGHCTIEGSSR GPMKLIGMHSEMVLDNLCPKEKNYEWSFIQCPACQCNHGHTCINNNVCEQCKNLTTGKQCQDCMPGYGD PTNGGQCTACTCSGHANIChLHTGKCFCTKGKIKGDQCQLCDSENRYVGNPLRGTCYCKYSLIDYQFTFSL LQEDDRHITAIFIANPEQVRKNLDISINASNNFNLNITWSVGSAGTISGEETSIVSKNNIKEYRDSFSYEK FNFRSNPNITFYVYVSNFSPWPIKIQSVKSIYF

15 The disclosed NOV2 amino acid sequence has 703 of 1197 amino acid residues (58%) identical to, and 895 of 1197 amino acid residues (74%) similar to, the 1198 amino acid residue Attractin protein from human (SPTREMBL-ID:O75882) ($E = 0.0$), and 703 of 1197 amino acid residues (58%) identical to, and 895 of 1197 amino acid residues (74%) similar to, the 1198 amino acid residue human soluble Attractin-1 protein (patp:AAY70689) ($E = 0.0$).

20 NOV2 is expressed in at least the following tissues: Brain, Kidney, Muscle, Pancreas, Prostate, Uterus, Breast, Colon, Ovary, and Liver. In addition, the sequence is predicted to be expressed in the following tissues because of the expression pattern of (GENBANK-ID: AF119821) a closely related attractin homolog in mouse : Brain, Heart, Kidney, Liver, Lung, Skin, Spinal cord, and Pituitary.

NOV2 also has homology to the amino acid sequences shown in the BLASTP data listed in Table 2C.

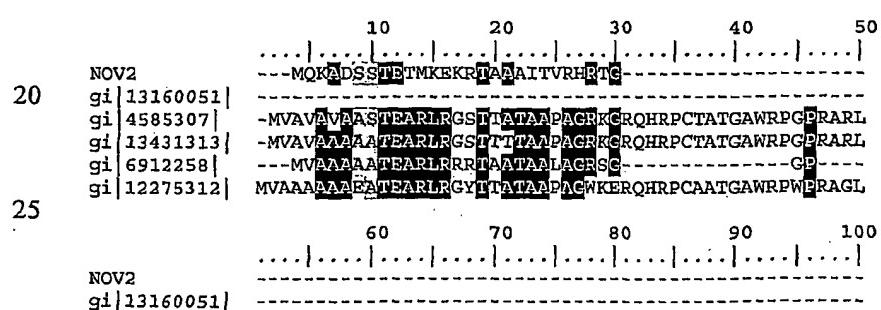
Table 2C. BLAST results for NOV2

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 13160051 emb CAC32456.1	dJ741H3.1.1 (attractin (with dipeptidylpeptidase IV activity) secreted isoform) [Homo sapiens]	1011	566/1015 (55%)	739/1015 (72%)	0.0
gi 4585307 gb AAD25372.1 AF119821_1	attractin [Mus musculus]	1428	677/1174 (57%)	865/1174 (73%)	0.0
gi 13431313 sp Q9WU60 ATRN_MOUSE	ATTRACTIN PRECURSOR (MAHOGANY PROTEIN)	1428	679/1174 (57%)	871/1174 (73%)	0.0
gi 6912258 ref NP_036202.1	attractin; attractin (with dipeptidylpeptidase IV activity); mahogany protein [Homo sapiens]	1198	703/1210 (58%)	894/1210 (73%)	0.0
gi 12275312 dbj BAB21018.1	attractin [Rattus norvegicus]	1275	680/1177 (57%)	870/1177 (73%)	0.0

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 2D.

Table 2D. ClustalW Analysis of NOV2

- 5
- 1) NOV2 (SEQ ID NO:7)
 - 2) gi|13160051|emb|CAC32456.1| dJ741H3.1.1 (attractin (with dipeptidylpeptidase IV activity) secreted isoform) [Homo sapiens] (SEQ ID NO:32)
 - 10 2) gi|4585307|gb|AAD25372.1|AF119821_1 attractin [Mus musculus] (SEQ ID NO:33)
 - 3) gi|13431313|sp|Q9WU60|ATRN_MOUSE ATTRACTIN PRECURSOR (MAHOGANY PROTEIN) (SEQ ID NO:34)
 - 4) gi|6912258|ref|NP_036202.1| attractin; attractin (with dipeptidylpeptidase IV activity); mahogany protein [Homo sapiens] (SEQ ID NO:35)
 - 15 5) gi|12275312|dbj|BAB21018.1| attractin [Rattus norvegicus] (SEQ ID NO:36)



	NOV2	GGQYAVEGHSAHITMELDSRDVVMMTIFGYSAIYGYSISIQEYHICNTWLS
	gi 13160051	-EQYAVVGHSAHIVTLKNGRVVMLVIFGHCPLGYVISVVOEYDLEKNTWS
	gi 4585307	-DQYAVVGHSAHIVTLASGRVVMLVIFGHCPLGYVISVVOEYDLEKNTWS
5	gi 13431313	-DQYAVVGHSAHIVTLASGRVVMLVIFGHCPLGYVISVVOEYDLEKNTWS
	gi 6912258	-EQYAVVGHSAHIVTLKNGRVVMLVIFGHCPLGYVISVVOEYDLEKNTWS
	gi 12275312	-DQYAVVGHSAHIVTLSSGRVVMLVIFGHCPLGYVISVVOEYDLEKNTWS
		510 520 530 540 550
10	NOV2	VPETRGALVQGGYCHTSVYDEITKSIIVHGGYKALPGNKVCHVDDLYRYD
	gi 13160051	ILHTQGALVQGGYCHSSVYDERTKALVHGGYKAFSANKYRLADDLYRYD
	gi 4585307	ILHTQGALVQGGYCHSSVYDERTKALVHGGYKAFSANKYRLADDLYRYD
	gi 13431313	ILHTQGALVQGGYCHSSVYDERTKALVHGGYKAFSANKYRLADDLYRYD
15	gi 6912258	ILHTQGALVQGGYCHSSVYDERTKALVHGGYKAFSANKYRLADDLYRYD
	gi 12275312	ILQTQGALVQGGYCHSSVYDERTKALVHGGYKAFSANKYRLADDLYRYD
		560 570 580 590 600
20	NOV2	VNTKWTILKESCHARYLISAVLINCAMLIFGGNTHNDTSLSGAKCFSS
	gi 13160051	VDTQMWTILKDSRFFRYLHTAVIVSGTMLVFGGNTHNDTSMSHGAKCFSS
	gi 4585307	VDTQMWTILKDSRFFRYLHTAVIVSGTMLVFGGNTHNDTSMSHGAKCFSS
	gi 13431313	VDTQMWTILKDSRFFRYLHTAVIVSGTMLVFGGNTHNDTSMSHGAKCFSS
	gi 6912258	VDTQMWTILKDSRFFRYLHTAVIVSGTMLVFGGNTHNDTSMSHGAKCFSS
	gi 12275312	VDTQMWTILKDSRFFRYLHTAVIVSGTMLVFGGNTHNDTSMSHGAKCFSS
25		610 620 630 640 650
	NOV2	DFAAYDIACPQ-WSAIVARSQIDATST--SHVQAEENRSMYFEGGFESSVLLN
	gi 13160051	DFMAYDIACDRWSVLPRPDLHHHDVNRFGHSAVLENSTMVFGGFNSLLL
	gi 4585307	DFMAYDIACDRWSVLPRPDLHHHDVNRFGHSAVLENSTMVFGGFNSLLL
30	gi 13431313	DFMAYDIACDRWSVLPRPDLHHHDVNRFGHSAVLENSTMVFGGFNSLLL
	gi 6912258	DFMAYDIACDRWSVLPRPDLHHHDVNRFGHSAVLENSTMVFGGFNSLLL
	gi 12275312	DFMAYDIACDRWSVLPRPDLHHHDVNRFGHSAVLENSTMVFGGFNSLLL
35		660 670 680 690 700
	NOV2	DILVFTKPPNCKAFRDEELCKNAAGPGIKCVANKN--HCESWESGNINN--I
	gi 13160051	DILVFTSEQCDahrseAACAAAGPGIRCVANTGSSOCISWALATEEQAEK
	gi 4585307	DILVFTSEQCDahrseAACAAAGPGIRCLWDTOSSRCISWELATEEQAEK
40	gi 13431313	DILVFTSEQCDahrseAACAAAGPGIRCVANTGSSOCISWALATEEQAEK
	gi 6912258	DILVFTSEQCDahrseAACAAAGPGIRCLWDTOSSRCISWELATEEQAEK
	gi 12275312	DILVFTSEQCDahrseAACAAAGPGIRCLWDTOSSRCISWELATEEQAEK
45		710 720 730 740 750
	NOV2	LRAKCFSKRNLCSDRCYRACASCTANTNGCQWCDKKCISANSNC--
	gi 13160051	LKSECFSKRKLTDHRCDCQHTDCYSCTANTNDCHWCND-HCVPRNHSCSEG
	gi 4585307	LKSECFSKRKLTDHRCDCQHTDCYSCTANTNDCHWCND-HCVPVNHSCTEG
50	gi 13431313	LKSECFSKRKLTDHRCDCQHTDCYSCTANTNDCHWCND-HCVPVNHSCTEG
	gi 6912258	LKSECFSKRKLTDHRCDCQHTDCYSCTANTNDCHWCND-HCVPRNHSCSEG
	gi 12275312	LKSECFSKRKLTDHRCDCQHTDCYSCTANTNDCHWCND-HCVPVNHSCTEG
55		760 770 780 790 800
	NOV2	MVSIFGYITLPSQFPFYCYKVALCASCCTAINGCQCD-DKKCIALPAS
	gi 13160051	QISIIFYENCPKDNPMPYYCNKKTSCRSCALDON-CQWEPRNOECIALPEN
	gi 4585307	QISIIFYENCPKDNPMPYYCNKKTSCRSCALDON-CQWEPRNOECIALPEN
	gi 13431313	QISIIFYENCPKDNPMPYYCNKKTSCRSCALDON-CQWEPRNOECIALPEN
60	gi 6912258	QISIIFYENCPKDNPMPYYCNKKTSCRSCALDON-CQWEPRNOECIALPEN
	gi 12275312	QISIIFYENCPKDNPMPYYCNKKTSCRSCALDON-CQWEPRNOECIALPEN
		810 820 830 840 850
65	NOV2	IICGIGAWHLSLKDQACIIRVNSSEFNYDNAKIYCVMILSGNIALSLTTISKEVEFVL
	gi 13160051	IICGIGAWHLVGNCSLKLITTAKENYDNAKLFCRNHNAFLASLTIQKKVEFVL
	gi 4585307	IICGIGAWHLVGNCSLKLITTAKENYDNAKLSCRNHNAFLASLTQSOKKVEFVL
	gi 13431313	IICGIGAWHLVGNCSLKLITTAKENYDNAKLSCRNHNAFLASLTQSOKKVEFVL
	gi 6912258	IICGIGAWHLVGNCSLKLITTAKENYDNAKLFCRNHNAFLASLTQSOKKVEFVL
70	gi 12275312	IICGIGAWHLVGNCSLKLITTAKENYDNAKLSCRNHNAFLASLTQSOKKVEFVL

	860	870	880	890	900	
	DEI-----QKYTCQKVSPPVGLRKINISYWGWEDEMSPTNTLQLWLPGE					
5	NOV2	KQLRIMQSSQSMSKLTLTPNVGLRKINVSYWCWEDMSPTNSLLQWMPSE				
	gi 13160051	KQLRIMQSSQSMSKLTLTPNVGLRKINVSYWCWEDMSPTNSLLQWMPSE				
	gi 4585307	KQLRIMQSSQSMSKLTLTPNVGLRKINVSYWCWEDMSPTNSLLQWMPSE				
	gi 13431313	KQLRIMQSSQSMSKLTLTPNVGLRKINVSYWCWEDMSPTNSLLQWMPSE				
	gi 6912258	KQLRIMQSSQSMSKLTLTPNVGLRKINVSYWCWEDMSPTNSLLQWMPSE				
	gi 12275312	KQLRIMQSSQSTSKLTLTPNVGLRKINVSYWCWEDMSPTNSLLQWMPSE				
10		910	920	930	940	950
	PNDSGFCAYLERAAGAVGLKANPCTSMANGLVCEKFVNQNARPCCKPCSLR					
	NOV2	PSDAGFCGILSEPSTRGLKAATCINPLNGSVCERPAHSAKQCRTPCALR				
	gi 13160051	PSDAGFCGILSEPSTRGLKAATCINPLNGSVCERPAHSAKQCRTPCALR				
	gi 4585307	PSDAGFCGILSEPSTRGLKAATCINPLNGSVCERPAHSAKQCRTPCALR				
	gi 13431313	PSDAGFCGILSEPSTRGLKAATCINPLNGSVCERPAHSAKQCRTPCALR				
	gi 6912258	PSDAGFCGILSEPSTRGLKAATCINPLNGSVCERPAHSAKQCRTPCALR				
	gi 12275312	PSDAGFCGILSEPSTRGLKAATCINPLNGSVCERPAHSAKQCRTPCALR				
20		960	970	980	990	1000
	TSCSNCTSNGMECMWCSSMKQCVDSNAVYISFPYGCQCMEWYTMSCPPEN					
	NOV2	TACGECTSSSECNWCSNMKQCVDSNAVYASFPFGQCMEWYTMSCPPEN				
	gi 13160051	TACGECTSSSECNWCSNMKQCVDSNAVYASFPFGQCMEWYTMSCPPEN				
	gi 4585307	TACGECTSSSECNWCSNMKQCVDSNAVYASFPFGQCMEWYTMSCPPEN				
	gi 13431313	TACGECTSSSECNWCSNMKQCVDSNAVYASFPFGQCMEWYTMSCPPEN				
	gi 6912258	TACGECTSSSECNWCSNMKQCVDSNAVYASFPFGQCMEWYTMSCPPEN				
	gi 12275312	TACGECTSSSECNWCSNMKQCVDSNAVYASFPFGQCMEWYTMSCPPEN				
30	NOV2	CSGLRTGQCLEOPECGWCNDPSNTGRCIEGSSRCPMKE-----IGMH				
	gi 13160051	CSGYCTCSHCLQPQCGWCNDPSNTGKGCIEGSYKGPVKMPSQAFTGNF				
	gi 4585307	CSGYCTCSHCLQPQCGWCNDPSNTGKGCIEGSYKGPVKMPSQAAGNV				
	gi 13431313	CSGYCTCSHCLQPQCGWCNDPSNTGKGCIEGSYKGPVKMPSQAAGNV				
	gi 6912258	CSGYCTCSHCLQPQCGWCNDPSNTGKGCIEGSYKGPVKMPSQAFTGNF				
	gi 12275312	CSGYCTCSHCLQPQCGWCNDPSNTGKGCIEGSYKGPVKMPSQAFTGNF				
		1010	1020	1030	1040	1050
					
40	NOV2	HSEMLDTNLCPKEKNYEWFSIQCPCACQNGHSKTCINNNVCEQCKNLTTG				
	gi 13160051	YPOPLLNNSSMCLEDSRYNWSFIHCPACQCNHHSKTCINQSICEKCNLTTG				
	gi 4585307	YPOPLLNNSSMCLEDSRYNWSFIHCPACQCNHHSKTCINQSICEKCNLTTG				
	gi 13431313	YPOPLLNNSSMCLEDSRYNWSFIHCPACQCNHHSKTCINQSICEKCNLTTG				
	gi 6912258	YPOPLLNNSSMCLEDSRYNWSFIHCPACQCNHHSKTCINQSICEKCNLTTG				
	gi 12275312	YPOPLLNNSSMCLEDSRYNWSFIHCPACQCNHHSKTCINQSICEKCNLTTG				
45		1060	1070	1080	1090	1100
					
	NOV2	KQQODCMGYYGDPTNGGQCTACTCSGHANICHLHTGKCFCTTKGTKGD2				
	gi 13160051	KHCETCISGFYGDPTNGGKCOPCKCNHGASLCNTNTGKCFCTTKGVKGDE				
	gi 4585307	KHCETCISGFYGDPTNGGKCOPCKCNHGASLCNTNTGKCFCTTKGVKGDE				
	gi 13431313	KHCETCISGFYGDPTNGGKCOPCKCNHGASLCNTNTGKCFCTTKGVKGDE				
	gi 6912258	KHCETCISGFYGDPTNGGKCOPCKCNHGASLCNTNTGKCFCTTKGVKGDE				
	gi 12275312	KHCETCISGFYGDPTNGGKCOPCKCNHGASLCNTNTGKCFCTTKGVKGDE				
55		1110	1120	1130	1140	1150
					
	NOV2	KQQODCMGYYGDPTNGGQCTACTCSGHANICHLHTGKCFCTTKGTKGD2				
	gi 13160051	KHCETCISGFYGDPTNGGKCOPCKCNHGASLCNTNTGKCFCTTKGVKGDE				
	gi 4585307	KHCETCISGFYGDPTNGGKCOPCKCNHGASLCNTNTGKCFCTTKGVKGDE				
	gi 13431313	KHCETCISGFYGDPTNGGKCOPCKCNHGASLCNTNTGKCFCTTKGVKGDE				
	gi 6912258	KHCETCISGFYGDPTNGGKCOPCKCNHGASLCNTNTGKCFCTTKGVKGDE				
	gi 12275312	KHCETCISGFYGDPTNGGKCOPCKCNHGASLCNTNTGKCFCTTKGVKGDE				
		1160	1170	1180	1190	1200
					
	NOV2	COLCDUSENRYQGNPLRGTCYCKYSLLIDYQFTFSLSQEDDRYYTAINFVA				
	gi 13160051	COLCEVENRYQGNPLRGTCY--YTLLIDYQFTFSLSQEDDRYYTAINFVA				
	gi 4585307	COLCEVENRYQGNPLRGTCY--YTLLIDYQFTFSLSQEDDRYYTAINFVA				
	gi 13431313	COLCEVENRYQGNPLRGTCY--YTLLIDYQFTFSLSQEDDRYYTAINFVA				
	gi 6912258	COLCEVENRYQGNPLRGTCY--YTLLIDYQFTFSLSQEDDRYYTAINFVA				
	gi 12275312	COLCEVENRYQGNPLRGTCY--YTLLIDYQFTFSLSQEDDRYYTAINFVA				
		1210	1220	1230	1240	1250
					
65	NOV2	NPEQVRKQNLDESINASNNFNLNITWVG-SAGTISGETSIVSKNNIKEY				
	gi 13160051	TPDEQNRDLDMFINASKNPNLNITWAISFSAGTOAGEEMPVVSKTNIKEY				
	gi 4585307	TPDEQNRDLDMFINASKNPNLNITWAISFPAGTOAGEEMPVVSKTNIKEY				
	gi 13431313	TPDEQNRDLDMFINASKNPNLNITWAISFPAGTOAGEEMPVVSKTNIKEY				
	gi 6912258	TPDEQNRDLDMFINASKNPNLNITWAISFSAGTOAGEEMPVVSKTNIKEY				

40 Tables 2E-I list the domain description from DOMAIN analysis results against NOV2. This indicates that the NOV2 sequence has properties similar to those of other proteins known to contain this domain.

Table 2E Domain Analysis of NOV2

gnl|Smart|smart00034, CLECT, C-type lectin (CTL) or carbohydrate-recognition domain (CRD); Many of these domains function as calcium-dependent carbohydrate binding modules. (SEQ ID NO:67)
CD-Length = 124 residues, 100.0% aligned .
Score = 70.1 bits (170), Expect = 7e-13

45	Query:	708	C G E G W - S H I G D A C L R V N S S R E N Y D N A K L Y C V N L S G N L A S L T T S K E V E F V L D E I Q K Y T Q Q K	766
	Sbjct:	1	+ + ++ ++ + + + + + + + + + + ++	
50	Query:	767	V S P W V G L R K I N I - S Y W G W E D M S P F T N T I L Q W L P G E P N D S G F C A Y L E R A A V A G L K A N P C T S	825
	Sbjct:	61	+ + + . + + +	
	Query:	826	M A N G L V C E 833	
			+	
55	Sbjct:	118	- K L P F I C E 124	

Table 2F Domain Analysis of NOV2

gnl|Smart|smart00042, CUB, Domain first found in Clr, C1s, uEGF, and bone morphogenetic protein.; This domain is found mostly among developmentally-regulated proteins. Spermadhesins contain only this domain.. (SEQ ID NO:68)
CD-Length = 114 residues, 96.5% aligned
Score = 66.2 bits (160), Expect = 1e-11

Query: 58	RLTEPSGYLT--DGPINYKYKTKCTWLIEGPNA-VLRLRFNHFATE---CSWDHMYVYD 110
	+ + + + + + ++ ++ +
Sbjct: 4	TLTASSGTITSPNYPNSYPNNLNCVWTISAPPGYRIELKFDFDLESSDNCTYDYVEIYD 63
Query: 111	GDSIYAPIIASFSGLIVPEIRGNETVPPEVVTTSGYALLHFFSDAAYNLTGFNIFYSI 167
	+ + + + ++ + + + +
Sbjct: 64	GPSTSSPPLLGRFCGSELPP-----PIISSSSNSMTVTFVSDSSVQKRQFSARYSA 113

10

Table 2G Domain Analysis of NOV2

gnl|Smart|smart00042, CUB, Domain first found in Clr, C1s, uEGF, and bone morphogenetic protein.; This domain is found mostly among developmentally-regulated proteins. Spermadhesins contain only this domain.. (SEQ ID NO:68)
CD-Length = 114 residues, 96.5% aligned
Score = 66.2 bits (160), Expect = 1e-11

Query: 58	RLTEPSGYLT--DGPINYKYKTKCTWLIEGPNA-VLRLRFNHFATE---CSWDHMYVYD 110
	+ + + + + + ++ ++ +
Sbjct: 4	TLTASSGTITSPNYPNSYPNNLNCVWTISAPPGYRIELKFDFDLESSDNCTYDYVEIYD 63
Query: 111	GDSIYAPIIASFSGLIVPEIRGNETVPPEVVTTSGYALLHFFSDAAYNLTGFNIFYSI 167
	+ + + + ++ + + + +
Sbjct: 64	GPSTSSPPLLGRFCGSELPP-----PIISSSSNSMTVTFVSDSSVQKRQFSARYSA 113

20

Table 2H Domain Analysis of NOV2

gnl|Pfam|pfam00431, CUB, CUB domain. (SEQ ID NO:69)
CD-Length = 110 residues, 97.3% aligned
Score = 63.9 bits (154), Expect = 5e-11

Query: 58	RLTEPSGYLT--DGPINYKYKTKCTWLIEGPNAV-LRLRFNHFATE---CSWDHMYVYD 110
	+ + + + + + + + + ++ +
Sbjct: 4	VLTESSGSIISSPNDYPNPKECVWTRAPPGYRVELTFQDFDLEDHTCRYDYVEIRD 63
Query: 111	GDSIYAPIIASFSGLIVPEIRGNETVPPEVVTTSGYALLHFFSDAAYNLTGFNIFY 165
	+ + + + ++ ++ + + +
Sbjct: 64	GDGSSSSPPLLGRFCGSGPP-----EDIVSSSNRMTIKFVSDASVSKRGFKATY 110

30

Table 2I Domain Analysis of NOV2

gnl|Pfam|pfam00059, lectin_c, Lectin C-type domain. This family includes both long and short form C-type (SEQ ID NO:70)
CD-Length = 107 residues, 100.0% aligned
Score = 49.3 bits (116), Expect = 1e-06

The protein of invention is highly homologous to the protein attractin, which is a membrane-associated or secreted molecule (depending upon the splice variant) in activated T cells. It has a protease activity and is thought to modify the N-termini of cytokines and chemokines, enabling the cells to interact and form clusters. The mouse ortholog of soluble attractin has been demonstrated to play a role in obesity and metabolic regulation. The protein of invention shows characteristic domains involved in protein-protein interactions, such as the CUB domain and the kelch motif. It also shows the presence of 4 plexin repeats, a lectin C-type domain and two laminin EGF-like domains, thus sharing its domain structure with attractin. Although attractin is predicted to be localized in the mitochondrial matrix, like the protein of invention, it is either secreted or located as a transmembrane protein at the plasma membrane. The protein of invention may therefore have diverse physiological roles in the tissues that it is expressed.

Attractin is a rapidly upregulated membrane-associated molecule on activated T cells (Duke-Cohan JS, et al. *Adv Exp Med Biol* 2000;477:173-85). It is a member of the CUB family of extracellular guidance and development proteins, sharing with them a protease activity similar to that of Dipeptidyl peptidase IV (DPPIV/CD26). Most remarkably, and in sharp contrast to CD26, it is released from the T cell and is presumed to be a major source of a soluble serum-circulating attractin. Genomic sequencing reveals that the soluble form is not a proteolytic product of the membrane form, but is in fact the result of alternative splicing. Recent results prove that the loss of murine membrane attractin results in the mahogany mutation with severe repercussions upon skin pigmentation and control of energy metabolism. In each of these latter instances, there is a strong likelihood that attractin is moderating the interaction of cytokines with their respective receptors. Attractin is likely performing a similar function in the immune system through capture and proteolytic modification of the N-termini of several cytokines and chemokines. This regulatory activity allows cells to interact

and form immunoregulatory clusters and subsequently aids in downregulating chemokine/cytokine activity once a response has been initiated. These two properties are likely to be affected by the balance of membrane-expressed to soluble attractin.

Attractin was initially identified as a soluble human plasma protein with dipeptidyl peptidase IV activity that is expressed and released by activated T lymphocytes. It has also been identified as the product of the murine mahogany gene with connections to control of pigmentation and energy metabolism. (Tang W et al., Proc Natl Acad Sci U S A 2000 May 23;97(11):6025-30). The mahogany product, however, is a transmembrane protein, raising the possibility of a human membrane attractin in addition to the secreted form. The genomic structure of human attractin reveals that soluble attractin arises from transcription of 25 sequential exons on human chromosome 20p13, where the 3' terminal exon contains sequence from a long interspersed nuclear element-1 (LINE-1) retrotransposon element that includes a stop codon and a polyadenylation signal. The mRNA isoform for membrane attractin splices over the LINE-1 exon and includes five exons encoding transmembrane and cytoplasmic domains with organization and coding potential almost identical to that of the mouse gene. The relative abundance of soluble and transmembrane isoforms measured by reverse transcription-PCR is differentially regulated in lymphoid tissues. Because activation of peripheral blood leukocytes with phytohemagglutinin induces strong expression of cell surface attractin followed by release of soluble attractin, these results suggest that a genomic event unique to mammals, LINE-1 insertion, has provided an evolutionary mechanism for regulating cell interactions during an inflammatory reaction.

The Mahogany/Attractin gene (Atrn) has been proposed as a downstream mediator of Agouti signaling because yellow hair color and obesity in lethal yellow (A(y)) mice are suppressed by the mahogany (Atrn(mg)) mutation. (Lu Xy et al., FEBS Lett 1999 Nov 26;462(1-2):101-7). The present study examined the distribution of Atrn mRNA in the brain and spinal cord by *in situ* hybridization. Atrn mRNA was found widely distributed throughout the central nervous system, with high levels in regions of the olfactory system, some limbic structures, regions of the brainstem, cerebellum and spinal cord. In the hypothalamus, Atrn mRNA was found in specific nuclei including the suprachiasmatic nucleus, the supraoptic nucleus, the medial preoptic nucleus, the paraventricular hypothalamic nucleus, the ventromedial hypothalamic nucleus, and the arcuate nucleus. These results suggest a broad spectrum of physiological functions for the Atrn gene product.

Completely different lines of experimentation have identified attractin, a protein that seems to have multiple roles in regulating physiological processes. (Jackson IJ Trends Genet

1999 Nov;15(11):429-31). It affects the balance between agonist and antagonist at receptors on melanocytes, modifies behaviour and basal metabolic rate, and mediates an interaction between activated T cells and macrophages. It may well be a target for development of drugs to treat obesity.

5 Agouti protein and agouti-related protein are homologous paracrine signalling molecules that normally regulate hair colour and body weight, respectively, by antagonizing signalling through melanocortin receptors. (Gunn TM, et al., Nature 1999 Mar 11;398(6723):152-6). Expression of Agouti is normally limited to the skin, but rare alleles from which Agouti is expressed ubiquitously, such as lethal yellow, have pleiotropic effects
10 that include a yellow coat, obesity, increased linear growth, and immune defects. The mahogany (mg) mutation suppresses the effects of lethal yellow on pigmentation and body weight, and results of our previous genetic studies place mg downstream of transcription of Agouti but upstream of melanocortin receptors. Here positional cloning was used to identify a candidate gene for mahogany, Mgca. The predicted protein encoded by Mgca is a 1,428-amino-acid, single-transmembrane-domain protein that is expressed in many tissues, including
15 pigment cells and the hypothalamus. The extracellular domain of the Mgca protein is the orthologue of human attractin, a circulating molecule produced by activated T cells that has been implicated in immune-cell interactions. These observations provide new insight into the regulation of energy metabolism and indicate a molecular basis for crosstalk between
20 melanocortin-receptor signalling and immune function.

Attractin is a normal human serum glycoprotein of 175 kDa that is rapidly expressed on activated T cells and released extracellularly after 48-72 hr. (Duke-Cohan JS et al., Proc Natl Acad Sci U S A 1998 Sep 15;95(19):11336-41). Attractin has been cloned and, in its natural serum form, it mediates the spreading of monocytes that become the focus for the clustering of nonproliferating T lymphocytes. There are two mRNA species with
25 hematopoietic tissue-specific expression that code for a 134-kDa protein with a putative serine protease catalytic serine, four EGF-like motifs, a CUB domain, a C type lectin domain, and a domain homologous with the ligand-binding region of the common gamma cytokine chain. Except for the latter two domains, the overall structure shares high homology with the
30 *Caenorhabditis elegans* F33C8.1 protein, suggesting that attractin has evolved new domains and functions in parallel with the development of cell-mediated immunity.

The disclosed NOV2 nucleic acid of the invention encoding a Attractin-like protein includes the nucleic acid whose sequence is provided in Table 2A or a fragment thereof. The invention also includes a mutant or variant nucleic acid any of whose bases may be changed

from the corresponding base shown in Table 2A while still encoding a protein that maintains its Attractin -like activities and physiological functions, or a fragment of such a nucleic acid. The invention further includes nucleic acids whose sequences are complementary to those just described, including nucleic acid fragments that are complementary to any of the nucleic acids 5 just described. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications. Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject. In the mutant or variant nucleic acids, and their complements, up to about 29% percent of the 10 bases may be so changed.

The disclosed NOV2 protein of the invention includes the Attractin -like protein whose sequence is provided in Table 2B. The invention also includes a mutant or variant protein any 15 of whose residues may be changed from the corresponding residue shown in Table 2B while still encoding a protein that maintains its Attractin -like activities and physiological functions, or a functional fragment thereof. In the mutant or variant protein, up to about 43% percent of the residues may be so changed.

The NOV2 nucleic acids and proteins of the invention are useful in potential 20 therapeutic applications implicated in Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neurodegeneration, Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney 25 disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalceimia, Diabetes, Pancreatitis, Obesity, Endometriosis, Infertility, Hirschsprung's disease, Crohn's Disease, Appendicitis, Muscular dystrophy, Lesch-Nyhan syndrome, Myasthenia gravis, Cirrhosis, Liver failure, Breast cancer, Ovarian cancer, Prostate cancer, Uterine cancer and/or other pathologies/disorders. The NOV2 nucleic acid encoding 30 Attractin-like protein, and the Attractin-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

NOV2 nucleic acids and polypeptides are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or

diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-NOVX Antibodies" section below. The disclosed NOV2 protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated NOV2 epitope is from about amino acids 1 to 20. In another embodiment, a NOV2 epitope is from about amino acids 50 to 130. In additional embodiments, NOV2 epitopes are from about amino acids 140 to 150, from about 180 to 380, from about amino acids 400 to 500, from about amino acids 530 to 550, from about amino acids 580 to 680, from about amino acids 700 to 740, from about amino acids 760 to 780, from about amino acids 820 to 900, and from about amino acids 950 to 1200. These novel proteins can be used in assay systems for functional analysis of various human disorders, which are useful in understanding of pathology of the disease and development of new drug targets for various disorders.

NOV3

15 NOV3 includes three novel Insulin Like Growth Factor Binding Protein Complex-Acid Labile Subunit (IGFBP-ALS)-like proteins disclosed below. The disclosed sequences have been named NOV3a and NOV3b.

NOV3a

20 A disclosed NOV3a nucleic acid of 6201 nucleotides (also referred to as 124217931_EXT) encoding a novel Kinase-like protein is shown in Table 3a. An open reading frame was identified beginning with a ATG initiation codon at nucleotides 57-59 and ending with a TGA codon at nucleotides 6199-6201. The start and stop codons are in bold letters.

Table 3A. NOV3a Nucleotide Sequence (SEQ ID NO:8)

<pre> ATGTTGAAGTCAAAATGGAGCGCGGAATCCCTTGGATGCTGGTCTGCTGAACCCATTGCCAGCCGGGC CTCCAGGCTGAATCTGTCTTCCAGGGAAACACCCTTTATGACTAACAGCAGATGTCCTCTTCCC GAGAAGGGATATTAGATGCCCTTCTTCTTCTTGAAAGAATGCAGTCAGCCTGCTCTGATGAAAGATTAAG CACGTGAGCAACTTGTCCGGAAAGTGTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTCGGCAA GGACTTGCAGACTCAGAACCTTGATGACTTGTGTCACTTGCTGAAGTCAGGAGCTTAAGAGGAAAGCAA CCGGGGACATCTATGCTATGAAAGATGAAAGAAGAGAAGGCTTATGGCCCGAGGAGCAGGTTTCAATT GAGGAAGAGCGGAACATATTATCTCGAGCACAAGCCGTGATCCCCAAATTACAGTATGCCCTTCAGGA CAAAATCACCTTATCTGTGATGGAATATCAGCCTGGAGGGACTTGTGTCACTTTGAATAGATATG AGGACCAGTTAGATGAAAACCTGATAACAGTTTACCTAGCTGAGCTGATTTGGCTGTCACAGCGTTCA CTGATGGGATACGTGCATCGGGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCT GGTGGATTGGATCTGCCGCAAAATGAAATTCAAACAGGTGAATGCCAAACTCCGATTGGGACCCAG ATTACATGGCTCTGAAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACTGTGAC TGGTGGCTAGGGCGTGATTGCCATGAGATGATTATGGGAGATCCCCCTTCAGAGGGAAACCTCTGC CAGAACCTCAATAACATTATGAATTTCAGCGGTTTTGAAATTTCAGATGACCCCAAAGTGAGCAGTG ACTTTCTTGATCTGATTAAGCTTGATGTCAGGAGACTGAAGTTGAAGGTCTTGCTGC CATCCTTCTCTAAATTGACTGGAACAAACATTGTAACGCTCCCTCCCCCTTCGTTCCACCCCTCAA </pre>
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CAGCACGGGAGAGAGCGTCCCCGGAGGCTGTTGAAGACAGCAGCAGGGCCGGCTGCCTGGGGAG
CCGTGAGGACCCCGCTTCCCAGGTGACAAGGTGAGGCAGCATTCGAGGCCTGTGTCTGTGCGGAG
GCCAGGAGTGAATTGGGAACTGA

The disclosed NOV3a nucleic acid sequence maps to chromosome 13 and has 5518 of 6158 bases (89%) identical to rho/rac-interacting citron kinase (Crik) mRNA from *Mus musculus* (GENBANK-ID:AF086824) (E = 0.0).

- 5 A disclosed NOV3a protein (SEQ ID NO:9) encoded by SEQ ID NO:8 has 2066 amino acid residues, and is presented using the one-letter code in Table 3B. Signal P, Psort and/or Hydropathy results predict that NOV3a does not have a signal peptide, and is likely to be localized to the nucleus with a certainty of 0.9800. In other embodiments NOV3a is also likely to be localized to microbody (peroxisome) with a certainty of 0.3000, to the
10 mitochondrial membrane space with a certainty of 0.1000, or to the lysosome (lumen) with a certainty of 0.1000.

Table 3B. Encoded NOV3a protein sequence (SEQ ID NO:9).

MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFTQQQMSPSLSREGILDALFVLFECSQPALMKIK
HVSNFVRKCSDTIAELQELQPSAKDFEVRSLSVCGHFAEVQVVREKATGDIYAMKVMKKALLAQEQVGSFF
EEERNILSRSTSPWIPOQYAFQDKNHLYLMEYQPGDILLSLLNRYEDQLDENLIQFYLAELIILAVERHSVH
LMGYVHRDIKPENILVDRTGHIKLUVDFGSAAKMNSNKVNALKLIGTPDYMMAPEVLTVMNGDGKGTYGLDCD
WWSVGVIAYEMIYGRSPFAEGTSARTFNNIMFQRFLKFPDDPKVSSDFLTLIQSLLCGQKERLKFEGLCC
HFFFFSKIDWMNIRNAPPFFVPTLKSDDTSNFDPEPKNSWVSSSPCOLSPSGFSGEELPFGFSYSKALGI
LGRSESVVSGLSPAKTSSMEKKLLIKSKELQDSQDKCHKMEQEMTRLHRRVSEVEAVLSQKEVELKASET
QRSLLEQDLATYITECSSLRSLSQARMEVSQEDDKALQLLHDIREQSRKLQEIKEQFYQAQVEEMRLMMN
QLEEDLVSAARRSDLYESLRESLIAEEFKRKATECQHKLLKAKDQGKPEVGEYAKLEKINAEEQQLKIQE
LQEKKLEKAVKASTATELLQNIRQAKERARRELEKLQNLREDSESEGIRKKLVEAERRHSLLENKVKRLETME
RRENRLKDDIQTKSQQIQQOMADKTLEELKEHREAQVSQAHQLEVHLKQKEQHYEEKIKVILDNQIKKDLADKE
TLENMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLSEQRIVELSEANKLAANSSLFTQRNMKAQEEMISE
LRQQKFYLETQAGKLEAQNRKLEQLEKISHQDHSDKNRLLTELETRLIREVSLHEHEEQKLELKROQTELQLS
LQERESQTLAQARAALESQRQAKTLEETTAEEIQLAHTHRKATDHPSTPATQRQFDALRNSCTVITDLEEQL
NQLTEDNAELNNQNMFYQSLQQLDEASGANDREVQLRSEVDHLRRETEIREDMLTSQKQTMEALKTTCTMLEE
QVMDLEALNDELLERKERQWEAWRSVLGDEKSQFECRVRRELQRLDTEKQSRARADQRITESRQVVELAVKE
EKAELIALQQALKEQKLKAESLSDKLNDLEKKHAMLEMNARSILQQKLETERELKQRLLEEQAKLQQQMDLQ
KNHIFRLTQGLQEAQALDRADLLKTERSDELYQLENIQVLYSHEKVKMEGTISQQTKLIDFLQAKMDQPAKKK
KVPQYNEKLALKEKCARCAELEELQKTRIELRSAREEEAHRKATDHPSTPATQRQIAMSATVRSP
EHQPSAMSLIAPPSSRRKESSTPEEFSSRRLKERMHHNI PHRFNVGLNMRATKCAVCLDTVHFGRQASKCLE
CQVMCHPKCSTCLPATCGLPAEYATHFTBAFCRDKMNSPGLQTKREPSSSLHELEGWMKVPRNNKRGQQGWDR
KYIVLEGSKVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELANTAKADVPYILKMEISHPTTCW
PGRTLYLLAPSFPDKQRWVTALESVAVGRVSREKAADAKLLGNSLLKLEGDDRLLDMNCLPFSQDVVLV
GTEEGLYALNVLKNSLTHVPGIGAVFQIYIKDLEKLMIAGEERALCLVDVKKVKQSLAQSHLPQPDFIS
PNIFEAVKGKCHLFAGKCIENGLCICAAMPSVNLRYNENLSKYCIRKEIETSEPCSCSIHFTNYSILIGTN
KFYEIDMKQYTLEBEFLDKNDHSLAPAVFAASSNSFPVSIVQVNSAGQREELYLLCFCHEFGVFVDSYGRRSRT
DDLKWSRLPFLAFAYREFYLFVTNFNSLEVIEIQARSSAGTPARAYLDIPNPRYLGPAISSGAIYIASSYQD
KLRVICCKGNLKVESGTEHHRGPSTSRRSPNKGPPTYNEHITKRVASSPAPPEGPSHPREPSTPHRYREG
RTELRRDKSPGRPLEREKSPGRMLSTRRERSPGRLFEDSSRGRLPAGAVRTPLSQVNKVRQHSEACVVAE
ARSIDLGN

- 15 The disclosed NOV3a amino acid has 1969 of 2053 amino acid residues (95%) identical to, and 2009 of 2053 amino acid residues (97%) similar to, the 2055 amino acid residue rho/rac-interacting citron kinase (Crik) protein from *Mus musculus* (SPTREMBL-ACC:O88938) (E= 0.0).

TaqMan expression data for NOV3a is found below is Example 2.

NOV3b

A disclosed NOV3b nucleic acid of 6189 nucleotides (designated CuraGen Acc. No. 5 CG106764-01) encoding a novel RHO/RAC-interacting citron kinase-like is shown in Table 3C. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TAA codon at nucleotides 6160-6162. A putative untranslated region downstream from the termination codon is underlined in Table 3C, and the start and stop codons are in bold letters.

10

Table 3C. NOV3b Nucleotide Sequence (SEQ ID NO:10)

```

ATGTTGAAGTCAAATATGGAGCGCGGAATCCTTGGATGCTGGCTGCTGAACCCATTGCCAGCCGGGCCTCC
AGGCTGAATCTGTTCTCCAGGGAAACCCCTTATGACTCAACAGCAGATGTCCTCTTCCCAGAAGGG
ATATTAGATGCCCTCTTGTCTTGAAGAGATGCAAGTCAAGCTGAGTCTGATGAAAGATTAACCACTGAGCAAC
TTTGTCCGGAAGTGTGTCACCATAGTGCTGAGTTACAGGGCTCCAGCCTCGGAAAGGACTTCAAGTCAAGTCAAG
AGTCTGTAGGGTGTGGTCATTTGCTGAGGTGAGAGAGAAAGCAACGGGGACATCTATGCTATG
AAAGTGTAGAGAAGAACGCTTATTGCCCCAGGAGCAGGTTCACTTTTGAAGGAAGAGCGGAACATATTATCT
CGAAGCACAGCCCGTGGATCCCCAATTACAGTATGCCCTTCAGGACAAAATCACCTTATCTGGTGATGGAA
TATCAGGCCGAGGGACTTGCTGCACTTTGAATAGATATGAGGACCAAGTGAATGAAAACCTGATAACAGTTT
TACCTAGCTGAGCTGATTGGCTTACAGGCTTCATCTGATGGGATACGTCATGGGACATCAAGCTGAG
AACATTCTCGTGGCCACAGGACATCAAGCTGGTGGATTGGGATCTGCCGAAAATGAATTCAACAAG
GTGAATGCCAAACTCCGATTGGGACCCCGATTACATGCCCTGAGTGTGATGAAACGGGGATGG
AAAGGCACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGCGTATGCCCTATGAGATGATTATGGGAGATCC
CCCTTCGAGAGGGAAACCTGCCCAGAACCTCAATAAACATTATGAATTTCAGCGCTTTTCAAAATTCAGAT
GACCCCAAAAGTGAGCAGTCACTTCTGATTGCAAGCTGGCCTTGGGAGGACTGAAAGAGAGACTGAAGTTT
GAAGGCTTTGCTGCCATCTTCTCTCAAATTGACTGGAAACAACTCTGAAACGCTCCCTCCCCCTCGTT
CCCAACCTCAAGTCTGAGCATGACACCTCAAATTGATGAAACAGAGAAATCTGGGGTTTCATCTCTCCG
TGCCAGCTGAGCCCCCTCAGGCTTCTGGGTGAAGAACCTGCCGTTGTGGGTTTCGTACGCAAGGCACTGGG
ATTCTGGTAGATCTGACTGTTGTGTCGGGCTGGACTCCCTGCCAAGACTAGCTCCATGAAAAGAAACTT
CTCATCAAAGCAAAAGACTACAAGACTCTGAGCAACTGTCACAAGCTGGGAGGAAATGACCCGGTTACAT
CGGAGAGTGTGAGGGTGGAGGCTGTGCTTAGTCAAGAGGGTGGAGCTGAAGGCTCTGAGACTCAGAGATC
CTCTGGAGGAGGACCTGACATCACAGAATGCACTAGCTTAAAGGAAAGTTGGAGCAAGCAGGATG
GAGGTGTCCAGGAGGATGACAACAAACACTGACGCTTCTCCATGATACTAGAGACAGGCCGAAGCTCCAAGAA
ATCAAAGAGCAGGAGTACCAAGGCTCAAGTGGAAAGAAATGAGGTTGATGATGAATCAAGTGGAAAGGGATCTGTC
TCAGCAAGAAGACGGAGTCACTCAGAATCTGAGCTGAGAGACTCTGGCTTCTGCTGAAGAATTCAGCGG
AAAGGCACAAATGTCAGCATAAACTGTGAGGCTAAGGATCAGGGAAACGCTTGGAGAAGTGGAGAATATGCCA
CTGGACAAAGTCAATCTGAGGAGCAGCTTCAAGGACCTCAAAGAGAACTGGAGAAGCTTGTAAAGC
AGCACGGACCCACCGAGCTGCTGAGAATATGCCACAGCAAAGGAGCAGGCCAGAGGGAGCTGGAGAGCTG
CAGAACCGAGAGGATTCTCTGAGGATCATGAGCATCAGAAAAGACTGGTGGAAAGCTGAGGAAACGCCGATCTCTGGAG
AACAAAGGTAAGAGACTAGAGACATGGAGCGTAGAGAAAACAGACTGAAGGATGACATCCAGACAAAATCCAA
CAGATCCACGAGATGGCTGATAAAATTCTGGAGCTGCAAGAGAAACATGCCAGGCCAAGTCTCAGCCAGCAC
CTAGAAGTGCACCTGAAAGGAGCAGCAACTGAGGATGAGGAAAGGAGCTGGAGAAGCTGGAGAGCTG
GACCTGGCTGAAAGGAGACACTGGAGAAGATGAGCATGAGAGACAGGGAGGCCATGAGAAAGGGAAAATT
CTCAGCGAACAGAAGGGATGATCAATGCTATGGATTTCAAGGATCAGATCCCTGGAAACAGGGATGTGGAACTG
TCTGAAGCCAATAAACTTCTGAGCAATAGCAGTCTTCTCCAAAGGAAACATGAAGGCTTGGAGGAGGAAACCGAAAAGTGGAG
TCTGAGACTCTCAGGCAACAGAAATTCTGGAGACACAGCTGGAGACAGGCTGGAGGAGCTTCCGAGGCCAGA
GAGCTGGAGAGGACACAGCAGAAGCTGAAGAGGAGATCCAGGCACTCACGGCAATAGAGATGAAATCCAGCGC
AAATTGATGCTCTTCGTAACAGCTGACTGTGATCACAGACCTGGAGGGAGCACTTAAACAGCTGACCCAGGAC
AACGCTGAACCTCAACACAAAATTCTCACTTGTCAAACAACTGAGAGACAGGGAGGCCATGAGAAAGGGAAAATT
GTACAACCTGCGAAGTGGAGGACATCTGGCGGGAGATCAGGAAACGAGAGATGAGCTTACCGCAGAG
CAAACGATGGAGGCTCTGAGAACACAGCTGACCTGGAGGAACAGAGCAGGGCGAGAGCCGATCAGCGGATCACCGAG
GAGCTGCTAGAAAAAGGGCGAGTGGAGGCTGGAGGAGCTGGAGGAGCTGGAGGAGCTGGAGGAGCTGGAGTGT
CGGGTTCCAGGAGCTGAGGGATGCTGGACACCGAGAACAGAGCAGGGCGAGAGCCGATCAGCGGATCACCGAG
TCTCGCCAGGTGGTGGAGCTGGCAGTGAAGGAGCACAAAGGCTGAGATCTCGCTCTGAGCAGGCTCTCAAAGAG

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CAGAAGCTGAAGCCGAGAGCCTCTCTGACAAGCTCAATGACCTGGAGAAGAAGCATGCTATGCTTGAATGAAT
GCCCGAAGCTTACAGCAGAAGCTGGAGACTGAAACGAGAGCTAAACAGAGGCTTCTGGAAGAGCAAGCCAATTAA
CAGCAGCAGATGGACCTGCAGAAAAATCACATTTCGCTGACTCAAGGACTGCAAGAAGCTTAGATCGGCT
GATCTACTGAAGACAGAAAGAGTGACTTGGAGTATCAGCTGAAAACATTCAAGGTGCTCTATTCTCATGAAAAG
GTGAAAATGGAAGGCACATTTCTCAACAAACCAAACCTATTGATTTCTGCAAGCCAATTGGACCAACCTGCT
AAAAGAAAAAGGTGCCCCTGCACTGAGTACAATGAGCTGAAGCTGGCCCTGGAGAAGGAGAAAGCTCGCTGTGAGAG
CTAGAGGAAGCCCTTCAGAACACCGCATTGAGCTCCGGCCGGAGGAAGCTGCCACGCCAAAGCAACG
GACCACCCACACCCATCCACGCCAGCCACCGCAGGGCAGCAGATGCCATGCTGCCATCGCGGTGCGCAGAG
CACCAAGCCAGTGCATGAGCCTGCTGGCCCCGCATCAGCCGAGAAAGGAGTCTCAACTCCAGAGGAATT
AGTCGGCGCTTAAAGGAACCATGCAACCAAAATTCCTACCGATTCAACGTAGGACTGAACATGCGAGCCACA
AAGTGTGCTGTGCTGGATAACCGTGCACCTTGGACGCCAGGATCAGATGCTAGAATGTCAGGTGATGTGT
CACCCCAAGTGTCTCACGTGCTGGCCAGCCTGCGCTGCTGCTGCAATATGCCACACACCTCACCGAGGCC
TTCTGCGGTGACAAAATGAATCTCCAGGTCTCCAGACAAAGGAGCCAGCAGCAGCTGCACTTGAAGGGTGG
ATGAAGGTGCCAGGAATAACAAACGAGGACAGCAAGGCTGGACAGGAAGTACATTGTCCTGGAGGGATCAAAA
GTCCTCATTTATGACAATGAAGCCAGAGAAGCTGGACAGAGGCCGGTGAAGAAATTGAGCTGTGCTTCCCGAC
GGGGATGTATCTATTATGCTGGCCGCTTGGCTGCACTCCGCAAATACAGGCCAGATGTCCTACATACATA
CTGAAGATGGAATCTCACCCGCAACACCACCTGCTGGCCGGAGAACCCCTACTTGTAGCTCCAGCTTCCCT
GACAAACAGCGCCTGGGTACCCGCTTAGAATCAGTTGTCGAGGTGGAGAGTTCTAGGAAAAGCAGAAGCT
GATGCTAAACTGCTTGGAAACTCCCTGCTGAAACTGGAGGTGATGACCGCTAGACATGAACGTGACGCTGCC
TTCAGTGACCAAGGTAGTGTGGTGGGACCCGAGGAAGGCTCTACGCCCTGAATGCTTGAAAAACCTCCCTAAC
CATGTCCTCAGGAAATTGGAGCAGTCCTCCAAATTATATCAAGGACCTGGAGAAGCTACTCATGATAGCAGGT
GAAGAGCGGGCAGTGTCTGGACGCTGAAGAAAAGTGAACACAGTCCCTGGCCAGTCCCACCTGCTGGCCAG
CCCGACATCTCACCCAAACATTGAGCTGCAAGGCTGCCCCTGCACTTGTGGGGCAGGCAAGATGAGAACGGG
CTCTGCATCTGTCAGCCACCCGCAACAGCTCTCATCTCCGCTACACGAAAACCTCAGCAAATACTGCATC
CGGAAAGAGATAGAGACCTCAGAGCCCTGAGCTGTATCCACTTCACCAATTACAGTATCCTCATGGAAACCAAT
AAATTCTACGAAATCGACATCAGCAGTACACGCTGAGGAATTCTGGATAAGAAATGACCATTCCTGGCACCT
GCTGTCTTGGCCCTCTTCAACAGCTCCCTGCTCAATCAGTGCAGGGCAGGCAACAGGGCAGGGCAGGAGAGG
TACTTGCTGTCTTCCAGAATTGGAGTGTCTGGATTCTTACGGAAAGACGTAGCCACAGAGGATCTCAAG
TGGAGTCCTTACCTTGGCTTGCCTACAGAGAACCTTACAGTTGTTGACCCACTCAACTCTGAGTA
ATTGAGATCCAGCACGCTCTCAGCAGGGACCCCTGCCAGCGTACCTGGACATCCGAACCCCGCTACCTG
GGCCCTGCCATTCTCAGGAGCGATTACTTGGCTCTCATACAGGAAATTAAAGGTATTGCTGCAAG
GGAAACCTCAGTGAAGGAGTCCGGCAGTGAACACCCACGGGGCCCTGCACTCCCGCAGCAGCCCCAACAGCGA
GGCCCAACCCAGTACAACAGCAGCACATCACAGCGCTGGCCCTCAGGGCAGGGCAGGCTGGCAGGGCAC
CCGGAGAGCAGCACACCCCCACCGTACCGCAGGGCAGGGCAGGCTGGCAGGGACAAGTCTCTGGCCG
CCCCCTGGAGCGAGAGAAGTCCCCCGGGCGATGCTCAGCACCCGGAGAGAGCGGTCCCCGGAGGCTTTGAA
GACAGCAGCAGGGCCGGCTGCCCTGGAGGAGCCCCGCTGCTCCAGGTGAACAAGGTGTGGGACCA
TCTTCAGTATAATCTCAGCCAGAAAACCAACTCCTCA

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The disclosed NOV3b nucleic acid sequence of this invention has 2894 of 2908 bases (99%) identity with KIAA1531 mRNA from Homo sapiens (GENBANK-ID: AB040964) (E = 0.0).

5 A NOV3b polypeptide (SEQ ID NO:11) encoded by SEQ ID NO:10 is 2053 amino acid residues and is presented using the one letter code in Table 3D. The SignalP, Psort and Hydropathy, Psort, and/or SignalP data suggest that the NOV3b protein has no signal peptide and may be localized to nucleus with a certainty of 0.9800. In other embodiments, NOV3b may also be localized to the microbody (peroxisome) with a certainty of 0.300, the
10 mitochondrial matrix space with a certainty of 0.100 or the lysosome (lumen) with a certainty of 0.100.

Table 3D. Encoded NOV3b protein sequence (SEQ ID NO:11)

```

MLKFKYGARNPLDAGAAEPIASRASRLNLFQQGKPPMTQQQMSPLSREGILDAFLFVLFEECSQPALMKIKHV
SNFVRKCSDTIAELQELQPSAKDFEVRSLSVCGGHFAEVQVVREKATGDIYAMKVMKKALLAQEQVSFFEEER
NILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNRYYEDQLDRLNLIQFYLAELILAVHSVHLMGYVH
RDIKPENILVDRTRGHIKLVDGFSAAKMSNKVNALKLIGTPDYMPEVLTVMNGDGKGTYGLDCDWWSVGVIA

```

YEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDL1QSLLCGQKERLKFEGLCCHPFFSKIDWN
 NIRNAPPPVPTLKSDDDTSNFDEPEKNSWSSSPCOLSPSGFSGEELPFVGFYSKALGILGRSESVVSGLD
 SPAKTSSMEKKLLIKSKELQDSQDKCHKMEQEMTRLHRRVSEVEAVLSQKEVELKASETQRSLLEQDLATYIT
 ECSSLKRSLEQARMEVSQEDDKALQLLHDIREQSRKLQ3IKEQEYQAQVEEMRLMMNOLEEDLVSARRSDLY
 ESELRESIRAAEEFKRKTECQHLLKAKDQKPEVGEYAKLEKINAEEQQLKIQELQEKLEKAVKASTATEL
 LQNIRQAKERARELEKLQNREDSSEGIRKKLVEAERRHSLENVKVRLETMERRENRLKDDIQTQKSQQIQQM
 ADKILEELEKHREAQVSAQHLEVHLKQKEQHYBEKIKVLDNQIKKDLADKETLENMORHEEEAHKGKILSE
 OKAMINADS KIRSLEQRIVELSEANKLAANSSLFTQRNMKAQEEMISELRRQQKFYLETQAGKLEAQNRKLEE
 QLEKISHQDHSDKNRLLERETRLETRLREVSLHEEQKLELKROLTELQLSLQERESQITALQAARAALESQLROAK
 TELEETTAEEETIQLALTHERDEIGRKFDALRNSCTITDLEEQLNQLTEDNAELNNQNFTLSKQLDEASGAN
 DEIVQLRSEVDHLRREITEREMQLTSQKTMCTMLLEQVMDLEALNDELLEKERQWEAWRSVLGDEK
 SQFECRVRELQRMIDTEKQSRARADQRTESRQVVELAVKEHAEILQALKEQQLKAESLSDKLNDEKK
 HAMLEMNARSLLQQQKLETERELKQLLEEQAKLQQQMDLQKNHIFRITOGLQEAQDRADLLKTERSDLEYQLEN
 IQVLYSHEKVMEGTISQQTKLIDFLQAKMDQPAKKKKVPLQYNEKLALKEKARCAELEALQKTRIELRS
 AREEEAAHRKATDHPHPSTPATRQQIAMSIAVRSPHQPSAMSLLAPPSSRKESTPPEEFSSRLKERMHHNI
 PHRFNVGLNMRATKCAVCLDTVHFGRAASKCLECQVMCHPKCSTCLPATCGLPAEYATHPTEAFCRDKMNSPG
 LQTKEPSSSLHLEGWMVKPRNNKRGQWDRKYIVLEGSKVLIYDNEAREAGQRPEEFELCLPDGVSIHGA
 VGANSELANTAKADVPIYLKMESHPTTCWPGRTLYLLAPSFPDKQRWVTALESVVAGGRVSREKAEDAKLLG
 NSLLKLEGDDRLDMNCNTLPFSQDVVLVGTEEGLYALNVLKNSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA
 LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAVKGCHLFAGKTIENGCLICAAMPSKVVILRYNENLSKYCIRK
 EIFTSEPCSCIHFNTNSILIGTNKPYEIDMKQTYTLEELDKNDHSIAPAFASNSFPVSIQVQNSAGQREE
 VLLCFHEFGVFVDSYGRRSRTDDLKWSRPLAFAYREPYLFVTHFNLSLEVIEQARSSAGTPARAYLDIPNPR
 YLGPAISGAIYLAASSYQDKLRLVICCKGNLVKESGTTEHHRGPSTSRSSPNKRGPTYNEHTKRVASSPAPPE
 GPSPHPREPSTPHRYREGTELRRDKSPGRPLEREKSPGRMLSTRRERSPGRLFEDSSRGRLPAGAVRTPLSQV
 NKVWDQSSV

The disclosed NOV3b amino acid sequence has 638 of 647 amino acid residues (98%) identical to, and 643 of 647 amino acid residues (99%) similar to, the KIAA1531 PROTEIN of 1060 amino acid residue prekallikrein-like protein from Homo sapiens (BAA96055) (E = 0.0).

5 NOV3b is expressed primarily in normal brain but not in other normal tissues. Lower expression is seen in several tumor types.

NOV3b also has homology to the amino acid sequences shown in the BLASTP data listed in Table 3E.

Table 3E. BLAST results for NOV3b

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 14768010 ref XP_045786.1	citron (rho-interacting, serine/threonine kinase 21) [Homo sapiens]	883	849/883 (96%)	849/883 (96%)	0.0
gi 6225217 sp O14578 CTRO_HUMAN	CITRON PROTEIN	1286	1165/1286 (90%)	1165/1286 (90%)	0.0
gi 4589542 dbj BAA76793.1	KIAA0949 protein [Homo sapiens]	940	887/940 (94%)	887/940 (94%)	0.0
gi 3360514 gb AAC27933.1	Citron-K kinase [Mus musculus]	1641	1476/1683 (87%)	1490/1683 (87%)	0.0
gi 1345860 sp P49025 CTRO_MOUSE	CITRON PROTEIN	1597	1427/1589 (89%)	1442/1589 (89%)	0.0

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 3F.

Table 3F. ClustalW Analysis of NOV3

	NOV3a	PFAEGTSARTFNNIMNFQRFLKFPPDPKVSSDFLDLTIQSLLCGQKERLKFEGLCCHPPFS	360
	NOV3b	PFAEGTSARTFNNIMNFQRFLKFPPDPKVSSDFLDLTIQSLLCGQKERLKFEGLCCHPPFS	360
5	gi 14768010 ref	-----	1
	gi 6225217 sp o	-----	1
	gi 4589542 dbj	-----	1
	gi 3360514 gb A	-----	1
	gi 1345860 sp P	-----	1
10		370 380 390 400 410 420	
	NOV3a	KIDWNNIRNAPPFVPTLKSDDDSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFSY	420
	NOV3b	KIDWNNIRNAPPFVPTLKSDDDSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFSY	420
15	gi 14768010 ref	-----	1
	gi 6225217 sp o	-----	1
	gi 4589542 dbj	-----	1
	gi 3360514 gb A	-----PFVPTLKSDDDSNFDEPEKNSWVSSVCQLSPSGFSGEELPFVGFSY	48
	gi 1345860 sp P	-----	1
20		430 440 450 460 470 480	
	NOV3a	SKALGILGRSESVVSGLDSPAQTSSMBKKLLIKSKELQDSQDKCHKMEQEMTRLHRRVSE	480
	NOV3b	SKALGILGRSESVVSGLDSPAQTSSMBKKLLIKSKELQDSQDKCHKMEQEMTRLHRRVSE	480
	gi 14768010 ref	-----	1
	gi 6225217 sp o	-----	1
25	gi 4589542 dbj	-----	1
	gi 3360514 gb A	SKALGILGRSESVVSLDSPA KVSSMBKKLLIKSKELQDSQDKCHKMEQEMTRLHRRVSE	108
	gi 1345860 sp P	-----MLLGEEM-----MEQEMTRLHRRVSE	22
30		490 500 510 520 530 540	
	NOV3a	VEAVLSQKEVELKASETQRSLLEQDLATYITECSSLKRSL EQARMEVVSQEDDKALQLLHD	540
	NOV3b	VEAVLSQKEVELKASETQRSLLEQDLATYITECSSLKRSL EQARMEVVSQEDDKALQLLHD	540
	gi 14768010 ref	-----	1
	gi 6225217 sp o	-----	1
35	gi 4589542 dbj	-----	1
	gi 3360514 gb A	VEAVLSQKEVELKASETQRSLLEQDLATYITECSSLKRSL EQARMEVVSQEDDKALQLLHD	168
	gi 1345860 sp P	VEAVLSQKEVELKASETQRSLLEQDLATYITECSSLKRSL EQARMEVVSQEDDKALQLLHD	82
40		550 560 570 580 590 600	
	NOV3a	IREQSRKLQEIKEQYQAQVEEMRLMMNQLEEDLVSARRRS DLYESELRESRLAAEEFKR	600
	NOV3b	IREQSRKLQEIKEQYQAQVEEMRLMMNQLEEDLVSARRRS DLYESELRESRLAAEEFKR	600
	gi 14768010 ref	-----	1
	gi 6225217 sp o	-----	1
45	gi 4589542 dbj	-----	1
	gi 3360514 gb A	IREQSRKLQEIKEQYQAQVEEMRLMMNQLEEDLVSARRRS DLYESELRESRLAAEEFKR	228
	gi 1345860 sp P	IREQSRKLQEIKEQYQAQVEEMRLMMNQLEEDLVSARRRS DLYESELRESRLAAEEFKR	142
50		610 620 630 640 650 660	
	NOV3a	KATECQHKLLKAKDQGKPEVGEYAKLEKINAEQQLKIQELQEKLEKAVKASTATELLQN	660
	NOV3b	KATECQHKLLKAKDQGKPEVGEYAKLEKINAEQQLKIQELQEKLEKAVKASTATELLQN	660
	gi 14768010 ref	-----	1
	gi 6225217 sp o	-----	1
55	gi 4589542 dbj	-----	1
	gi 3360514 gb A	KANE CQHKLMKAKDQGKPEVGEYSKLEKINAEQQLKIQELQEKLEKAVKASTATELLQN	288
	gi 1345860 sp P	KANE CQHKLMKAKDQGKPEVGEYSKLEKINAEQQLKIQELQEKLEKAVKASTATELLQN	202
60		670 680 690 700 710 720	
	NOV3a	IRQAKER AERELEKLQNREDSSSEGIRKKLVEAERRHSL ENVKRLETMERRENRLKDDI	720
	NOV3b	IRQAKER AERELEKLQNREDSSSEGIRKKLVEAERRHSL ENVKRLETMERRENRLKDDI	720
	gi 14768010 ref	-----	1
	gi 6225217 sp o	-----	1
65	gi 4589542 dbj	-----	1
	gi 3360514 gb A	IRQAKER AERELEKLHNREDSSSEGIKKKLVEAEE-----	322
	gi 1345860 sp P	IRQAKER AERELEKLHNREDSSSEGIKKKLVEAERRHSL ENVKRLETMERRENRLKDDI	262
70		730 740 750 760 770 780	

	NOV3a	QTKSQQIQQMADKILELEEKHREAQVSAQHLEVHLKQEYEEKIKVLDNQIKKDLADK	780
	NOV3b	QTKSQQIQQMADKILELEEKHREAQVSAQHLEVHLKQEYEEKIKVLDNQIKKDLADK	780
5	gi 14768010 ref	-----	1
	gi 6225217 sp o	-----	13
	gi 4589542 dbj	-----	1
	gi 3360514 gb A	LEEKHREAQVSAQHLEVHLKQEYEEKIKVLDNQIKKDLADK	366
	gi 1345860 sp P	QTKESEQIQQMADKILELEEKHREAQVSAQHLEVHLKQEYEEKIKVLDNQIKKDLADK	322
10		790 800 810 820 830 840	
	NOV3a	EILENMMQRHEEEAHKGKILSEOKAMINANDSKIRSLEQRIVELSEANKLAANSSLFTQ	840
	NOV3b	EILENMMQRHEEEAHKGKILSEOKAMINANDSKIRSLEQRIVELSEANKLAANSSLFTQ	840
	gi 14768010 ref	-----	1
	gi 6225217 sp o	-----	73
15	gi 4589542 dbj	-----	1
	gi 3360514 gb A	ESLENMMQRHEEEAHKGKILSEOKAMINANDSKIRSLEQRIVELSEANKLAANSSLFTQ	426
	gi 1345860 sp P	ESLENMMQRHEEEAHKGKILSEOKAMINANDSKIRSLEQRIVELSEANKLAANSSLFTQ	382
20		850 860 870 880 890 900	
	NOV3a	RNMKAQEEQMISLERQQKFYLETOAGKLEAQNRKLEEQLEKISHQDHSDKRNRLLELETRLR	900
	NOV3b	RNMKAQEEQMISLERQQKFYLETOAGKLEAQNRKLEEQLEKISHQDHSDKRNRLLELETRLR	900
	gi 14768010 ref	-----	1
	gi 6225217 sp o	-----	133
25	gi 4589542 dbj	-----	1
	gi 3360514 gb A	RNMKAQEEQMISLERQQKFYLETOAGKLEAQNRKLEEQLEKISHQDHSDKSRRLLELETRLR	486
	gi 1345860 sp P	RNMKAQEEQMISLERQQKFYLETOAGKLEAQNRKLEEQLEKISHQDHSDKSRRLLELETRLR	442
30		910 920 930 940 950 960	
	NOV3a	EVSLHEEQKLELKQLTELQLSQLQERESQLTALQAARAALESQLRQAKTELEETTAEAE	960
	NOV3b	EVSLHEEQKLELKQLTELQLSQLQERESQLTALQAARAALESQLRQAKTELEETTAEAE	960
	gi 14768010 ref	-----	1
	gi 6225217 sp o	-----	193
35	gi 4589542 dbj	-----	1
	gi 3360514 gb A	EVSLHEEQKLELKQLTELQLSQLQERESQLTALQAARAALESQLRQAKTELEETTAEAE	546
	gi 1345860 sp P	EVSLHEEQKLELKQLTELQLSQLQERESQLTALQAARAALESQLRQAKTELEETTAEAE	502
40		970 980 990 1000 1010 1020	
	NOV3a	EEIQALTAAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEASG	1020
	NOV3b	EEIQALTAAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEASG	1020
	gi 14768010 ref	-----	1
	gi 6225217 sp o	EEIQALTAAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEASG	253
45	gi 4589542 dbj	-----	1
	gi 3360514 gb A	EEIQALTAAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEASG	606
	gi 1345860 sp P	EEIQALTAAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEASG	562
50		1030 1040 1050 1060 1070 1080	
	NOV3a	ANDEIVQLSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQVMDLEALNDELLEK	1080
	NOV3b	ANDEIVQLSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQVMDLEALNDELLEK	1080
	gi 14768010 ref	-----	1
	gi 6225217 sp o	ANDEIVQLSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQVMDLEALNDELLEK	313
55	gi 4589542 dbj	-----	1
	gi 3360514 gb A	ANDEIVQLSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQVMDLEALNDELLEK	666
	gi 1345860 sp P	ANDEIVQLSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQVMDLEALNDELLEK	622
60		1090 1100 1110 1120 1130 1140	
	NOV3a	ERQWEAWRSVLGDEKSQFECRVRELORMLDTEKOSRARADQRITESRQVVELAVKEHKAЕ	1140
	NOV3b	ERQWEAWRSVLGDEKSQFECRVRELORMLDTEKOSRARADQRITESRQVVELAVKEHKAЕ	1140
	gi 14768010 ref	-----	1
	gi 6225217 sp o	ERQWEAWRSVLGDEKSQFECRVRELORMLDTEKOSRARADQRITESRQVVELAVKEHKAЕ	373
65	gi 4589542 dbj	-----	27
	gi 3360514 gb A	ERQWEAWRSVLGDEKSQFECRVRELORMLDTEKOSRARADQRITESRQVVELAVKEHKAЕ	726
	gi 1345860 sp P	ERQWEAWRSVLGDEKSQFECRVRELORMLDTEKOSRARADQRITESRQVVELAVKEHKAЕ	682
70		1150 1160 1170 1180 1190 1200	

Tables 3G-K list the domain description from DOMAIN analysis results against NOV3b. This indicates that the NOV3 sequence has properties similar to those of other proteins known to contain this domain.

Table 3G Domain Analysis of NOV3b

gnl|Pfam|pfam00780, CNH, CNH domain. Domain found in NIK1-like kinase, mouse citron and yeast ROM1, ROM2. Unpublished observations (SEQ ID NO:71)
CD-Length = 304 residues, 99.7% aligned
Score = 238 bits (607), Expect = 2e-63

Table 3H Domain Analysis of NOV3b

gnl|Smart|smart00220, S_TKc, Serine/Threonine protein kinases, catalytic domain; Phosphotransferases. Serine or threonine-specific kinase subfamily. (SEQ ID NO:72)
CD-Length = 256 residues, 100.0% aligned
Score = 230 bits (587), Expect = 5e-61

Table 3I Domain Analysis of NOV3b

gnl|Smart|smart00036, CNH, Domain found in NIK1-like kinases, mouse citron and yeast ROM1, ROM2; Unpublished observations. (SEQ ID NO: 73)
CD-Length = 301 residues, 99.7% aligned
Score = 226 bits (577), Expect = 8e-60

25	Query:	1619	DMNCTLPPSDQ--VVLVGTEEGLYALNVLKN--SLTHVPGIGAVFQIYIIKDLEKLLMIA + ++ + + + +++++ +	1674
	Subjct:	2	TAKWNHPICTCDAKILLVGTEEGLYVLNISDQHGTLIKEGRRSVTQIWVLEENNVLIMIS	61
	Query:	1675	GEERALC---LVDVKKKVQSLAQSHLPAQFDISPNIPEAVKGCCHLFGAGKIEMLCICAA ++ + + + + + + + ++ + + +	1731
30	Subjct:	62	GKKPQLYSHPLSALTE-KDALGSARLVRKVNLT-IPDVKGCHLCAVVNNGKRILFLCHA	119
	Query:	1732	MPSKVVIL-RYNENLSKYCIR----KEIETSEPCSCIHFTNY---SILIGTMKFYEIDM + + + + + + + + + +	1782
	Subjct:	120	LQSSVVLLOWYNPLKKFKLFKSKFLFPLISPVPVFELVSSSFELPGICIGSDK-NGGDV	178
35	Query:	1783	KQYTLLEEFLDKNDHSLAPAVFAASSNSFPVSIVQVNSAGQREEEYLLCFHEFGVVFVDSYG- + + + + + + + +	1841
	Subjct:	179	VQFH-QSLVSKEDLSLPFLSEETSSKPISVVQVP-----ADELLLCYDEFGVFNLYGM	231
40	Query:	1842	RRSRRTDDLKWSPRLPLAFAYREPYLFWTFHNSLEVIBIQARSSAGTPARAYLDIPNPRYLG + + + +	1901
	Subjct:	232	RRSRNPILHWEFMPESFAYHSPLLAFHDNGIEIRSIKTGELLQELADR--KTRKIRLLG	289
45	Query:	1902	PAISSLGAIYLLASSY 1915 +	
	Subjct:	290	S--SDRKILLSSSP 301	

Table 3J Domain Analysis of NOV3b

gnl|Pfam|pfam00069, pkinase, Protein kinase domain. (SEQ ID NO:74)
CD-Length = 256 residues, 100.0% aligned
Score = 189 bits (481), Expect = 1e-48

Table 3K Domain Analysis of NOV3b

gnl|Smart|smart00219, TyrKc, Tyrosine kinase, catalytic domain;
Phosphotransferases. Tyrosine-specific kinase subfamily. (SEQ ID
NO: 75)
CD-Length = 258 residues, 95.0% aligned
Score = 91.7 bits (226), Expect = 4e-19

25	Query:	104	GCGHFAEVQVREKATGDIYAMKVMKKALLAQE-QVSFFEEERNILSRSTSPWIPQLQY	162
	Sbjct:	8	+ + + + ++ + +	67
30	Query:	163	AHQDKNHLYLVMEYQPQGDLLSLLNRYEDQLDENLIQFYLAELI-LAVHSVHLMGYVHRD	221
	Sbjct:	68	++ + + + + + + + +	127
35	Query:	222	VCTEEEPLMIVMEYMEGGDLLDYLRKRNPKELSLSDLLSFALQIARGMEYLESKNFVHRD	279
	Sbjct:	128	IKPENILVDRTRGHIKLVDGSSAAKMNSNKVNALKPIGTPD--YMAPEVLTVMNQDGKGTY	181
40	Query:	280	LAARNCLVGENKTVKIADFGLARDLYDDYYRKKSPLRPIRWMAPESLK-----DGKF	338
	Sbjct:	182	+ + + + + + + + + + +	238
40	Query:	339	TSKSDVWSFGVLLWEIFTLGESEPVPGMSNEEVLEYLKKGYRLPQPPNCP---DEIYDLML	
	Sbjct:	239	SLLCGQ---KERLKFE 351 + +	
		Q--CWAEDPEDRPTFS 252		

Recent data shows the identification of a novel serine/threonine kinase belonging to the myotonic dystrophy kinase family (DiCunto et al. Eur J Immunol 2000 Dec;30(12):3403-10.). The kinase can be produced in at least two different isoforms: a approximately 240-kDa

protein (Citron Rho-interacting kinase, CRIK), in which the kinase domain is followed by the sequence of Citron, a previously identified Rho/Rac binding protein; a approximately 54-kDa protein (CRIK-short kinase (SK)), which consists mostly of the kinase domain. CRIK and CRIK-SK proteins are capable of phosphorylating exogenous substrates as well as of 5 autophosphorylation, when tested by *in vitro* kinase assays after expression into COS7 cells. CRIK kinase activity is increased several fold by coexpression of constitutively active Rho, while active Rac has more limited effects. Kinase activity of endogenous CRIK is indicated by *in vitro* kinase assays after immunoprecipitation with antibodies recognizing the Citron moiety of the protein. When expressed in keratinocytes, full-length CRIK, but not CRIK-SK, 10 localizes into corpuscular cytoplasmic structures and elicits recruitment of actin into these structures. The previously reported Rho-associated kinases ROCK I and II are ubiquitously expressed. In contrast, CRIK exhibits a restricted pattern of expression, suggesting that this kinase may fulfill a more specialized function in specific cell types.

T cell receptor (TCR) engagement increases integrin-mediated adhesion to APC, 15 resulting in the stabilization of the T cell. APC interaction and the close apposition of the two cell membranes. Engagement of either the TCR or CD3 chimeras with immobilized antibodies causes the rapid spreading of T cells in an integrin-independent fashion (Borroto et al. Eur J Immunol 1999 Nov;29(11):3609-20). This effect concurs with the polymerization of the actin cytoskeleton and is dependent on the integrity of the immunoreceptor tyrosine-based 20 activation motifs of the CD3 subunits. Expression of a dominant negative mutant of RhoA, as well as the Rho-specific inhibitor C3 toxin, abolished TCR-induced spreading. In contrast, constitutively active or dominant negative forms of Rac and Cdc42 did not affect cell spreading. Signals emanating from the TCR can directly induce T cell spreading, independently of integrins, and via a Rho-dependent reorganization of the actin cytoskeleton.

Motile lymphocytes adopt a polarized morphology with different adhesion molecules 25 (ICAM, CD43 and CD44) and ERM actin-binding proteins concentrated on the uropod, a slender posterior appendage with important functions in cell-cell interactions and lymphocyte recruitment. The role of Rho family of GTPases (Rho, Rac and Cdc42) in the control of lymphocyte polarity and migration has been studied by analyzing the effects of exogenously introduced Rho GTPase mutants. Transfection of T cell lines that constitutively display a 30 polarized motile morphology with activated mutants of RhoA, Rac1 and Cdc42 impaired cell polarization. A guanosine nucleotide exchange factor for Rac, Tiam-1, induced the same effect as activated Rac1. Conversely, dominant negative forms of the three GTP-binding proteins induced a polarized phenotype in constitutively round-shaped T cells with

redistribution of ICAM-3 and moesin to the uropod in an integrin-dependent manner. On the other hand, overexpression of dominant negative Cdc42 and activated mutants of all three Rho GTPases significantly inhibited SDF-1alpha-induced T cell chemotaxis. Together, these data demonstrate that Rho GTPases regulate lymphocyte polarization and chemokine-induced
5 migration, and underscore the key role of Cdc42 in lymphocyte directional migration.

Activated Rho GTPases trigger distinctive kinase cascades. In particular, ROCK binds to Rho, and its kinase activity is moderately stimulated by this association. The citron molecule (Madaule et al., 1995), a specific interactor of Rho and Rac, shares a significant degree of structural homology with ROCK; however, its lack of a kinase domain raised the
10 question of its biologic function. By PCR of a mouse primary keratinocyte cDNA library, Di Cunto et al. (1998) identified a novel serine/threonine kinase, CRIK (citron Rho-interacting kinase), belonging to the myotonic dystrophy kinase family. CRIK can be expressed as at least 2 isoforms, one of which encompasses the previously reported form of citron in almost its entirety. The long form of CRIK is a 240-kD protein in which the kinase domain is followed
15 by the sequence of citron. The short form, CRIK-SK (short kinase), is an approximately 54-kD protein that consists mostly of the kinase domain. CRIK and CRIK-SK proteins are capable of phosphorylating exogenous substrates as well as of autophosphorylation, when tested by *in vitro* kinase assays after expression into COS-7 cells. CRIK kinase activity is increased several-fold by coexpression of constitutively active Rho, while active Rac has more
20 limited effects. Kinase activity of the endogenous CRIK is indicated by *in vitro* kinase assays after immunoprecipitation with antibodies recognizing the citron moiety of the protein. When expressed in keratinocytes, full-length CRIK, but not CRIK-SK, localizes into corpuscular cytoplasmic structures and elicits recruitment of actin into these structures. The previously reported Rho-associated kinases ROCK1 and ROCK2 are ubiquitously expressed. Northern
25 blot analysis of mouse tissues revealed a restricted pattern of expression limited to keratinocytes, brain, spleen, lung, kidney, and an especially strong signal in testis. No expression was detectable in heart, liver, or skeletal muscle. The CRIK protein contains a kinase domain, a coiled-coil domain, a leucine-rich domain, a Rho-Rac binding domain, a zinc finger region, a pleckstrin homology domain, and a putative SH3-binding domain. Di Cunto et al. (1998) reported cloning the human homolog of the CRIK kinase domain. They stated that the human homolog of citron is contained within a PAC clone (GenBank GENBANK AC002563) mapping to chromosome 12q. By screening size-fractionated human brain cDNA libraries for cDNAs encoding proteins larger than 50 kD, Nagase et al. (1999) identified CRIK
30

as cDNA KIAA0949 (GenBank GENBANK AB023166). Di Cunto et al. (1998) mapped the human CRIK gene to chromosome 12q24.1-q24.3.

Di Cunto et al. (2000) generated mice deficient in citron kinase by targeted disruption. Citron-K^{-/-} mice grow at slower rates, are severely ataxic, and die before adulthood as a consequence of fatal seizures. Their brains display defective neurogenesis, with dramatic depletion of microneurons in the olfactory bulb, hippocampus, and cerebellum. These abnormalities arise during development of the central nervous system due to altered cytokinesis and massive apoptosis. Di Cunto et al. (2000) concluded that citron-K is essential for cytokinesis in vivo, in specific neuronal precursors only. Moreover, they suggested a novel molecular mechanism for a subset of human malformation syndromes of the central nervous system.

The disclosed NOV3 nucleic acid of the invention encoding a RHO/RAC-interacting citron kinase -like protein includes the nucleic acid whose sequence is provided in Table 3A or 3C or a fragment thereof. The invention also includes a mutant or variant nucleic acid any of whose bases may be changed from the corresponding base shown in Table 3A or 3C while still encoding a protein that maintains its RHO/RAC-interacting citron kinase -like activities and physiological functions, or a fragment of such a nucleic acid. The invention further includes nucleic acids whose sequences are complementary to those just described, including nucleic acid fragments that are complementary to any of the nucleic acids just described. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications. Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject. In the mutant or variant nucleic acids, and their complements, up to about 10% percent of the bases may be so changed.

The disclosed NOV3 protein of the invention includes the RHO/RAC-interacting citron kinase -like protein whose sequence is provided in Table 3B or 3D. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in Table 3B or 3D while still encoding a protein that maintains its RHO/RAC-interacting citron kinase -like activities and physiological functions, or a functional fragment thereof. In the mutant or variant protein, up to about 13% percent of the residues may be so changed.

The protein similarity information, expression pattern, and map location for the RHO/RAC-interacting citron kinase-like protein and nucleic acid (NOV3) disclosed herein suggest that NOV3 may have important structural and/or physiological functions characteristic of the citron kinase-like family. Therefore, the NOV3 nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications. These include serving as a specific or selective nucleic acid or protein diagnostic and/or prognostic marker, wherein the presence or amount of the nucleic acid or the protein are to be assessed, as well as potential therapeutic applications such as the following: (i) a protein therapeutic, (ii) a small molecule drug target, (iii) an antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) a nucleic acid useful in gene therapy (gene delivery/gene ablation), and (v) a composition promoting tissue regeneration in vitro and in vivo.

The NOV3 nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications implicated in various diseases and disorders described below. For example, the compositions of the present invention will have efficacy for treatment of patients suffering from asthma, arthritis, psoriasis, diabetes, and IBD, which require activated T cells, as well as diseases such as systemic lupus erythematosus that involve B cell activation, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Renal tubular acidosis, IgA nephropathy, Hypercalceimia, Lesch-Nyhan syndrome, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Endocrine dysfunctions, Obesity, Growth and Reproductive disorders Hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, allergies, immunodeficiencies, transplantation, Lymphaedema, Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host, Hirschsprung's disease, Crohn's Disease, Appendicitis Inflammatory bowel disease, Diverticular disease, and/or other pathologies. The NOV3 nucleic acid, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

NOV3 nucleic acids and polypeptides are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-NOVX Antibodies" section below. For example the disclosed NOV3 protein have multiple hydrophilic regions,

each of which can be used as an immunogen. In one embodiment, contemplated NOV3 epitope is from about amino acids 1 to 20. In another embodiment, a NOV3 epitope is from about amino acids 40 to 45. In additional embodiments, NOV3 epitopes are from about amino acids 110 to 150, from about amino acids 210 to 300, from about amino acids 410 to 900, from 5 about amino acids 950 to 1200, from about amino acids 1250 to 1300, from about amino acids 1310 to 1450, from about amino acids 1490 to 1520, from about amino acids 1650 to 1680, from about amino acids 1800 to 1820, from about amino acids 1900 to 1920 and from about amino acids 1980 to 2053. This novel protein also has value in development of powerful assay system for functional analysis of various human disorders, which will help in 10 understanding of pathology of the disease and development of new drug targets for various disorders.

NOV4

A disclosed NOV4 nucleic acid of 5691 nucleotides (designated CuraGen Acc. No. 15 105827550_EXT) encoding a novel Plexin-like protein is shown in Table 4A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TGA codon at nucleotides 5683-5685. A putative untranslated region downstream from the termination codon is underlined in Table 4A, and the start and stop codons are in bold letters.

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Table 4A. NOV4 Nucleotide Sequence (SEQ ID NO:12)

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ATGAAAGGCCATGCCCTGGAACTGGACCTGGCTTCTC1CCCACTCTCATGGTGCGCATGGGCTCTCCA
CTTGCTCACCGGGCAGCCAGCCCCGCTGTCAGAAGCAGCGGTCAATTGTCACATTCGAGGAAGCC
CGCCGAGGGTTTCATCAACTCTGGTGTGGATGAGAGGACAGGAACATTTACTTGGGGCCGTCAATCGG
ATTACAAGCTCTCCAGCAGCTGAAGGTCTGGTGACGCATGAGACAGGGCCGGACGAGGAACACCCCA
AGTGTACCCACCCCGCATGTCAGACCTGCAATGAGCCCTGACCAACCACAAATGTCAACAAGAT
GCTCTCATAGACTACAAGGAGAACAGGCTGATTGCCCTGGGAGCCTGTACAAAGGCATCTGCAAGCTG
CTGAGGCTGGAGGACCTCTCAAGCTGGGGCTTATCAAGAAGGAGCACTATCTGTCAAGGTGTCA
ACGAGAGCGGCTCAGTCCTGGAGTGTCTCCTACAGCAACCTGGATGACAAGCTGTTATTGCCAC
GGCAGTGGATGGGAAGCCCGAGTATTTCCCACCATCTCAGCCGGAAACTGACCAAGAACTCTGAGGCG
GATGGCATGTCGCAGCTCTTCCATGATGAGTTGTGGCTCGATGATTAAGATCCCTTCGACACCT
TCACCATCATCCCTGACTTGTATCTACTATGTCTATGGTTTAGCAGTGGCAACTTTGCTACTTTT
GACCCCTCAACCTGGAGATGGTGTCTCCACCGGCCACCCACCAAGGGAGCAGGTGTATAACATCCAAGCTC
GTGAGGCTTGCAGGAGGACACAGCCTCTCAACTCTTATGTAGAGGTGCCCATGGCTGTGAGCGCAGTG
GGGTGGAGTACCGCCCTGTCAGGCTGCTACTGTCAAAAGCGGGGGCGTGTGGCAGGACCCCTGG
AGTCCATCCAGATGATGACCTGCTCTCACCGCTTCTCCAAGGGCCAGAAGCGAAAATGAAATCCCTG
GATGAGTCGGCCCTGTGCACTTCACTTGAAGCAGATAATGACCCATTAAAGGAGCGGTGCAAGCTT
GTTACCGGGCGAGGGCACGGCTGGACCTGGCTGGCTCAAGGTGAAGGACATCCCCCTGCAGCAGTGGCT
CTTAACCATGGACATAACTCTGTGGCTGGACATGAATGCTCCCCCTGGAGTGTCCGACATGGTGGT
GGAATTCCCTCTTCAAGGAGAACGGGACCCCATGACCTCTGTCATGGCATAATGTCTAACAGAACACT
CTCTGGCTTGTGGGACCAAAGTGGCAAGCTGAAGAAGATCCGGGTGGATGGACCCAGGGCAACGC
CCTCCAGTATGAGACGGTGAGGTGGACCCGGCCAGTCCTCCGGATATGGCCTTCTCCAAGGAC
CACGAGCAACTCTACATCTGTCAGAGAGGAGCAGCTCACCAAGAGTCCCCCTGGAGTCTGTGGTCAAGTATC
AGAGCTGCGGGAGTGCTTGCTCAGGGGACCCCCACTGTGGCTGGTGTGCTGACAACACGTGCA
CCGGAGGAGCGGTGTGAGCGGTCAAGGAGCCCCGAGGTTGGCTGGAGATGAAGCAGTGTGTCGG
CTGACGGTCCATCCCAACATACTCCGCTCTCAGTACAACGTGCTGCTGGTCTGGAGACGTACAATG
TCCCGGAGCTGTCAGCTGGCGTCAACTGCACCTTGAGGACCTGTGAGAGATGGATGGCTGGTGGGG

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CAATCAGATCCAGTGTACTCCCCGTGAGCCAAGGAGGTGCCCGGATCATCACAGAGAATGGGGACAC
 CATGTCGTACAGCTCAGCTAAATCAAGGAGACCGCATGACCTTCGCGAGCACCAGCTTGTCTCT
 ACAATTCCAGCGTCACAATTCTGCTGTCTCGCGAGAGTCCATACCGCTGCACACTGGTGTAAATA
 CCGGCATGTCGACCCATGACCCAAAGACCTGCTCTCCAGGAAGGCCAGTGAAGCTGCCGAGGAC
 TGCCCCCAGCTGCTGCAGTGAGAAGATCTGGTGCCTGGAGGTGATCAAGGCTATCACGCTGAAGG
 CCAAGAACCTCCCCAGCCCCAGTCTGGCAGCGTGGCTACGAATGCACTCTCAACAACTCAGGGCAGCGA
 GCAGCGAGTGCCTCGCTCAACAGCTCCAGCTACAGTGCAGAACACCTCTTATTCCTATGAA
 GGGATGGAGATCAACAACTGCCGTGGAGTTGACAGTGTGTGGAACTGGCACTTCAACATTGACAAAC
 CAGCTCAGAAATAAGTCACCTCTACAGTGTGGAGGCCATGCGTGAAGAGCTGCCGCTGTGCTCAAGGC
 TGACCCAGACTTCGATGTGGTGGCCAGGGCCCAGGCCAGTGCACCCCTGCCAGCACTGCCCTGCC
 CAGGAGAGCCAGTGGCTGGACTGTCTGGTCCAAAAGCAAGTGCACAAACCCCGCATCACAGAGATAA
 TCCCCTGTAAGGGGGGGGCAACAGGCTACTATCGAGGGGAGAACCTGGGCTTGAATT
 TCGCGACATGCCCTCATGTCAGGTTGCTGGCTGGAGTGCAGCCCTTTAGTGGATGGTACATCCCT
 GCAGAAACAGATCGTGTGAGATGGGGAGGCCAACGGCCAGCATGCAAGGCTTCGTGGAGATCTCGC
 TGGCTGTGTGCCCTGAATTATGGCCCGTCTCACAGCTCTATTACTTCATGACACTGACTCTC
 AGATCTGAAGCCCAGCGGGGCCCAGTCCGAGGGGCCAACTGACCATCACAGGCAACCTGAAT
 CCCGGAACGCAAGCTGGTGTGATGTTGAAAGCAGCCCTGCTCTCCACAGGCGATCTCCATC
 TTGCTGCCAACACCATCTCATGAGATGAGAGTGAAGGTTGCTGGTGCAGGTGGACAGGGCAA
 GATCCACAGGACCTGGCTTCACTGAGTATGAGGACAGGACATGCGGATTGAGGCAAGATGGAC
 ATTGTCACTGAAACACACCCATGCCGTATGGGGACCCACCTGGACCTCATACAGAACCCCCAGATCC
 GTGCCAAGCATGGAGGGAGGAGCACATCAATATCTGTGAGGTCTGAAACGCTACTGAGATGACCTGCA
 GGGCCTCCCTCGTCTGGTCTGCAACCCAGTCAACACTGACCCGAGGGCCGAGGGAGTTGGCTT
 ATCCGACAACTGCCAGTCCCTGCTCATCTCAACAAAGCAACTTCCACTATATCCAAACCCGGTGT
 TTGAGGCTTTGGCTCCCTGAGGATCTGGAGCTCAAGGCTGGCACGCCATCATCTAAAGGGCAACAA
 CCTGATCCCCCTGCTGGCTGGGGCAACGTCAGACTACACTGTGCTGGTGGGAGAAGCCGTGC
 ACCGTGACCGTGTGAGATGTCCAGCTGCTCTGCGAGTCCCTCACCGCAGGCACAAAGTGATGG
 CCCGTGCTGGCATGGAGTACTCCCCGGGATGGTGTACATTCCCGGACAGCCGCTCAGCCTGCC
 CCCCATCGTCAGATCGCAGTGGCTGGCCCTCTCATCTTTCATCGTGGCCGTGCTCATGCCAT
 AAACCGCAACTCCGGAAAGTGAACCTCACGCTGAAGCCGTGCAAGTGCAGATGGACAACTGGAGTCCC
 CTGTGGCCCTGGAGTCAAGGAAGCCTTGGCAGCTCAGACGACATCATGAGCTGACAGTGCACCT
 GGATGGAGCCGGGATTCGGTCTGGACTATAGAACCTACACCATGGGGTGTCTTCCAGGAATTGAA
 GACCACCCCTGTCCTCGGGACCTTGAGGTCCGGGCTACCGGCAAGAGCGTGGAGAAAGGCTGAGC
 TCTTCGCCCCACTCAACAAACAGGTTCTGCTCTCCATGGTGTCTCATCGCAGCCTGGAGCTGGAG
 CTTCTCCATGCCAACCTGGCTGAGGACTGACTCATGAGCTGAGGAGTGTGAGCTGGAGTAG
 GCCACTGATGCTGAAGCAGCTGCTGGGACCTCATGACAACACCTGGAGAGCAAGAACCACTTA
 AGCTGCTCTCAGGAGGACTGAGTCACTGGCTGAGAAGATGCTGACCAATTGGTTTACTTCCCTCT
 CAAGTTCCCTCAAGGAGTGTGCTGGGAGGCCCTTCTCCATGGTGTGCTCATCAAGCAGCAGATGGAG
 AAGGGCCCATGACCCATCACGGGCAAGGGCGTACTCCCTGAGCAGGACAAGCTCATCCGCCAGC
 AGATTGACTACAACCCCTGGCTGAGGACTGAGTCAAGGAGAATATGAAATGAGCTGGGAGGTC
 AAAGATCTCAACTGACACCATCACTCAGGTCAGGAGAAGATTGGATGCTGGAGTGGGCAAGGATGA
 CTTTGCTCCACCGGCCAAACCTGCAAGATATGGATCTGGAGTGGGCAAGGAAGTGGGCAAGGATGA
 TCTTGAGGATGAAGACATCACCACCAAGATGAGAATGTTGAAGGCGACTGAACACACTGGCCACTA
 CCAGGTGCGAGATGGTTCCGTGGTGGCATTAAGTGTGAGGCTGAGGCTATAACGCACTGAAACAC
 TCCCGTCTCCGACGACCATCTGACCTCTGAGGAGTGGAGTGGAGCTGGAGCTGGGAGGTC
 TCCGCTCACGGACACCATGACTCTCTGACCTGGAGAGTGGAGTGGAGCTGGAGCTGGGAGGTC
 ACCCGTGGCTCTGCCCTGCCATCAACTACATGTTGAGCTCTCTGAGGACCATCTTCAGCAGGGAC
 TGGCATTGATGACCCGACCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
 ATGATCAAGAACCCGAGCTGGTGTGACATCCATAAGAACAGCATCACAGACGCTGCTCTCTG
 TGGCTCAGACCTTATGGACTCTTGTCTCACTGCTGAGGACACGGCTGGGAGGAGGACTGGCCTC
 GCTGCTGTATGCCAAGGACATCCCCAGCTACAAGAATTGGGAGGAGGAGGAGGAGGAGGAGGAG
 ATGCCAGGATCAGCGACCAAGACATGAACGCACTGGCTGAGCAGTCCCGGATGCACTGAATGAGT
 TCAACACCATGAGTGCACCTCAGAGATCTCTCTATGTGGGAAATAACAGCGAGGAGATCCTGGACC
 TCTGGACCCAGATGACCGAGTGTGGAGAGCAAACTGCCCTACAAACTAGAACAAAGTCATAACCC
 AGCTTAGACAGCTGAAATAAA

The nucleic acid sequence of NOV4, localized on chromosome 7, has 4004 of 5567 bases (71%) identical to a plexin-2 mRNA from mouse (GENBANK-ID: D86949) (E = 0.0).

A NOV4 polypeptide (SEQ ID NO:13) encoded by SEQ ID NO:12 is 1896 amino acid residues and is presented using the one letter code in Table 4B. Signal P, Psort and/or Hydropathy results predict that NOV4 has no signal peptide and is likely to be localized at the

plasma membrane with a certainty of 0.46. In other embodiments, NOV4 may also be localized to the endoplasmic reticulum (membrane) with a certainty of 0.1000, the endoplasmic reticulum (lumen) with a certainty of 0.1000, or the outside with a certainty of 0.1000.

5

Table 4B. NOV4 protein sequence (SEQ ID NO:13)

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MKAMPWNWTCLLSHLLMVGMSSTLITRQPAPLSQKQRSFVTFRGEPAEGFNHLVVDERTGHIYLGAVNRIYKL
SSDLKVLTHTGPDEDPKCYPPRIVQTNCNEPTTTNNVNKMILLDVKENRLIACGSILYQGICKLRLLEDLFK
LGEFYHKKEHYLSGVNESGSVFGVIVSYSNLDDKLFIATAVDGKPEYFPTTSSRKLTKNSEADGMFAYVFHDF
VASMKIPSDFTIIIPDFDIYVYGFSGNFVFLTLQPEMVSPPGSTTKEQVYTSKLVRLCKEDTAFNSVVEV
PIGERSGVSEYRLLQAAYLSKAGAVLGLRTGLGVHPDDDLIFTVFSKGQKRKMKSLLDESALCIPILKQINDRIKER
LQSCYRGEGLDLAWLKVKDIPCSSALLTIDDNFCGLDMNAPLGVSDMVRGIPVFTEDRDRMTSIAVYVKHNS
LAFAVGTGKGLKKIRVDGPRGNALQYETVQVVDPGPVLRDMAFSKDHQLYIMSERQLTRVPVSCGQYQSCGE
CLGSGDPHCGWCVLHNTCTRKERCSKEPDRFASEMKGCVRLTVPPNNISVSQYNVLLVLETYNVPELSAGVN
CTFEDLSEMGLVVGNGNQIQCYSPAVERPRIITENGDHVQLQKSKETGMTFASTSFVVFYNSCVHNSCLSCV
ESPYRCHWCKVRHVCTHDPKTCSFQERGVKLPCPQLLRVDKILVPEVIEKPIITKAKNLQPQSGQRGYECI
LNHQGSEQRVPALRFNSSSVQCQNTSYSYEGMEINNLPELTVVNGHFNIDNPAQNKVHLYKCCAMRESCGLC
LKADPDFACGWCQCPGQCTLRQHCPAQESQWLLELSGAKSKCTNPRITHIIPVTGPREGGTKVTRGENLGLEFR
DIASHVKVAGVECSPVLDGYIIPAEQIVCEMGEAKPSQHAGFVEICAVCRPEFMARSSQLYYFMTLTLSDLKPS
RGPMSSGGTQVTTGTLNAGSNVVMFGKQPCFLHRSPSYIVCNNTSSDEVLEMKVSVQVDRAKIHQDLVFOY
VEDPTIVRIEPEWSIVSGNTPIAVVGTHLTLQNPQIRAKHGGKEHINICEVLNATEMTQAPALALGPDHQSD
LTERPEEFGFILDNVQSLILLNKTNTFTYYPNPVFEAFGPGSILELKPGTPIILKGKNLIPPVAGGNVKLNYTVL
VGEKPCTVSDVQLLCESPNLIGRHVMARVGGMEYSPGMVIAPDPLSLPAIVSIAVAGGLIIFIIVAVLI
AYKRKSRESDLTLKRLQMMDNLESRVALECKEAFAELOTDIHELTSDLDGAGIIPFLDYRTYTMRLVFPGLIEDH
PVLRDLEVPGYRQERVEGKFLFAOLINNKVFLLSFIRTLESQRFSMRDRGNVASLIMTVLQSKLEYATDVLK
QLIADLIDKNLESKNHPKLLRRRTESVAEKMLTNWTFILLYKFLKECAPEPLFLSAIKQQMEKGPIDAITE
ARYSLSEDKLIRQDIDYKTLVLCVSEPDNANSPEVVKILNCDTIQVKEKILDIAFKNVPCSHRPKAADMDLE
WRQGSGARMILQDEDITTKIENDWKRLNLTQHYPDGSVVALVSKQVTAYNAVNNTSVSRSTSASKYENMIRYT
GSPDLSRSRTPMIITPDLESVGKVMWHLVKNHEHGDKEGDRGSKMVEIYLTRLLATKGTQKFVDDLFETTFST
AHRGSALPLA1KYMFDLDEQADKHG1HDHPVHRTWKSNCPLRFWNMKIKNPQFVFDIHKNSITDACLSVVAQ
TFMDSCSTSEHRLGKDSPSNKLLYAKD1PSVKNVVERYYSDIGKMPAISDQDMNAYLAEQSRMMNEFNTMSAL
SEIFSYVGKYSEBILGPLDHDQCGKQKLAYKLEQVITLMSLDSNk
```

The full amino acid sequence of the protein of the invention was found to have 1263 of 1857 amino acid residues (68%) identical to, and 1501 of 1857 amino acid residues (80%) similar to, the 1884 amino acid residue plexin-2 protein from mouse (SPTREMBL-P70207) 10 (E =0.0), and 364 of 801 amino acid residues (45%) identical to, and 520 of 801 amino acid residues (64%) similar to, the 2135 amino acid residue Human Plexin protein (patp:AAU00019) (E = 6^{-283}).

The disclosed NOV4 protein is expressed in at least the following tissues: fibroblast like synoviocytes (normal), fetal brain, adipose, microvascular endothelial cells-lung, 15 thalamus, fetal cerebral cortex, temporal lobe, parietal lobe, fetal cerebellum, and testis. TaqMan expression data for NOV4 is shown below in Example 2.

NOV4 also has homology to the amino acid sequences shown in the BLASTP data listed in Table 4C.

Table 4C. BLAST results for NOV4

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 13649119 ref XP_010150.2	SEX gene [Homo sapiens]	1871	1121/1846 (60%)	1413/1846 (75%)	0.0
gi 3413888 dbj BAA32308.1	KIAA0463 protein [Homo sapiens]	1963	1270/1870 (67%)	1508/1870 (79%)	0.0
gi 2134135 pir IS1553	Plexin - African clawed frog	1905	1220/1915 (63%)	1468/1915 (75%)	0.0
gi 14424639 gb AAH09343.1 AAH09343	Unknown(protein for IMAGE:4130636) [Homo sapiens]	813	641/810 (79%)	717/810 (88%)	0.0
gi 10047165 dbj BAB13376.1	KIAA1550 protein [Homo sapiens]	593	513/513 (100%)	513/513 (100%)	0.0

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 4D.

Table 4D ClustalW Analysis of NOV4

- 5 1) NOV4 (SEQ ID NO:13)
 2) gi|13649119|ref|XP_010150.2| SEX gene [Homo sapiens] (SEQ ID NO:42)
 3) gi|3413888|dbj|BAA32308.1| KIAA0463 protein [Homo sapiens] (SEQ ID NO:43)
 4) gi|2134135|pir||IS1553 Plexin - African clawed frog (SEQ ID NO:44)
 5) gi|14424639|gb|AAH09343.1|AAH09343 Unknown(protein for IMAGE:4130636) [Homo sapiens] (SEQ ID NO:45)
 6) gi|10047165|dbj|BAB13376.1| KIAA1550 protein [Homo sapiens] (SEQ ID NO:46)

10	10 20 30 40 50	
	
15	NOV4	
	----- ----- ----- ----- ----- ----- ----- -----	
	gi 13649119	----- ----- ----- ----- ----- ----- ----- -----
	gi 3413888	GFGRLPDSELRAGRGASRRPQQPAAAEVDRAGTEGQTDVAELESCEGQPG
	gi 2134135	----- ----- ----- ----- ----- ----- ----- -----
	gi 14424639	----- ----- ----- ----- ----- ----- ----- -----
	gi 10047165	----- ----- ----- ----- ----- ----- ----- -----
20	60 70 80 90 100	
	
25	NOV4	
	----- ----- ----- ----- ----- ----- ----- -----	
	gi 13649119	MKAMPWNWTCLLSHLLVMGMGSSTLLT
	gi 3413888	-----MP-----SVC-----LLLFLAVG-G
	gi 2134135	KVEQMSTHRSLRLLTAAPLSMEQRREPWRALEVDSDRSVVVLSVVVWVLLAPP
	gi 14424639	-----MLLHAERPLP----FHLWTFLVLLGSWIATGDG
	gi 10047165	----- ----- ----- ----- ----- ----- ----- -----
30	110 120 130 140 150	
	
35	NOV4	
	RQPAPLSQKRSFVTFRGEPAEGFWHLVVDERTGHYLYGAVNRIYKLSSD	
	gi 13649119	ALGNRPFPRAFVV--TDTTLTHLAVRVRTGEVFVGAVNRVFKLAPNLTELRL
	gi 3413888	AAGMPQFSTFHSENRDWTFNHLTVEQGTGAVVVGATNRVYKLTGNLTIQV
	gi 2134135	SP--KDFRTFTG--SDWSLTHLVEENKTGEVYVGATNRVYKLSNNLTLRL
	gi 14424639	----- ----- ----- ----- ----- ----- ----- -----
	gi 10047165	----- ----- ----- ----- ----- ----- ----- -----
40	160 170 180 190 200	
	
45	NOV4	
	LKVLTVTHETGPDDEDNEKCYPPIVQTCNEPLTTNNVKMLLIDYKENRL	
	gi 13649119	AHVIGPVEDMARCYPPFSMRVCAHRLAPVDNINKLIDYARRLIVACGS
	gi 3413888	AHKTGPEEDONKSCYPPLIVQPCSEVLTLNNVNKLIDYSENRLACGS
	gi 2134135	THVTGPVEONEKCYPPPSVQSCPHEGLITNNVNKLIDYSDNRLIACGS
	gi 14424639	----- ----- ----- ----- ----- ----- ----- -----
	gi 10047165	----- ----- ----- ----- ----- ----- ----- -----

210 220 230 240 250

	NOV4
	gi 13649119	IACGSLYQGICKLIRLEDFKLGEPEYHKKEHLSGVNESGSIVFGVIVSYS
	gi 3413888	IWQGICQFRLRDDLFLKLGEPEHHRKEHLSGAQEPDSMAGVIVBQGQQGPSK
5	gi 2134135	LYQGVCKLRLRDDLFLILVEPSHKKEHLSVNKTGTMYGVIVVRSEGEDGK
	gi 14424639	ASQGICQFRLRDDLFLKLGEPEHHRKEHLSVNESGTMMSGVILEVPNGQNK
	gi 10047165	-----
10		260 270 280 290 300
	NOV4
	gi 13649119	NLDDDKLFIATAVDGKPEYFPITSSRKLTKNSEADGMFAYVFHDEFVASMI
	gi 3413888	LFVGTAVDGKSEYFPTLSSRKLTSDEDSADMFSLVYQDEFVSSQIKIPSD
	gi 2134135	LFIGTAVDGKQDYFPTLSSRKLPDPESSAMLDYELHSDFVSSLKIPSD
15	gi 14424639	LFVGTPIDGKSEYFPTLSSRKLTGNEENAEMFGFVYQDEFVSSQLKIPSD
	gi 10047165	-----
20		310 320 330 340 350
	NOV4
	gi 13649119	KTPSDTFTIIPDFDIKYYVYGFSSGNFVYFLTQLOPEMVSPGSTTKEQVYT
	gi 3413888	TISLYPAPFDIYIYIGFVSASEFVYFLTQOLDTQOTLILDAGEKFFTSKIV
	gi 2134135	TIALVSHFDIYIYIGFASGGFVYFLTQPEPPKGVAINSAGDLFYTSRIV
25	gi 14424639	TISKFPTFDIYVYSESSEOFVYVYLTLQOLDTQLTSPDSTGEQFFTSKIV
	gi 10047165	-----
30		360 370 380 390 400
	NOV4
	gi 13649119	SKLVRLOKRDIAFNSYVEVPIGCERSGMEYRLLQPAVLSKAGAVLGRTLG
	gi 3413888	RMCAGDSEFYSYVEFPIGCSWRGVBEYRIVQSAHLAKPGLLLQAQALGVPAD
	gi 2134135	RLCKDDPKFHGSYVSLPFGCTRAGVEYRILQAAYLAKPGDSLQAQAFNITSQ
	gi 14424639	RLCVDDPKFYSYVEFPIGCMKDGVBEYRITODAYLSKPGKRLAKELGISER
35	gi 10047165	-----
40		410 420 430 440 450
	NOV4
	gi 13649119	VHPDDDFLFTVFSKGOKRKMKSLDE SALCIFILKONDEKNERLSCYRG
	gi 3413888	EDVLFTIIFSQGQKNRASPPQFLCLFTLSNNAHIREPIGSCYRGEGTL
	gi 2134135	DVDLFAIFI SKGOKQYHHPPDDSALCAFPIAENLOIKCRHOSCYDGEGL
	gi 14424639	EDILFTIIFSQGQKNRIPPKESVLCLFTLKKDKDIIKERIOTSCYPGDGKL
	gi 10047165	-----
45		460 470 480 490 500
	NOV4
	gi 13649119	EGTLDIAWLKVKDIPCSSALLTIDNF CGLDMNAPLCVSDMVRGIVPVTE
	gi 3413888	ALPWLINKELPCINTPMQINGNF CGLVLNQPIGGLVIEGLPLLLADSTDG
50	gi 2134135	ELNWLI GKD VQCTKAPVPIDDNF CGLDINQPIGGSTPVEGLTLYTTSRDR
	gi 14424639	SLPWLINKELGCINSPLQIDDNFCGQDFNQPPIGGTVTDEGTPLFLDKBDG
	gi 10047165	-----
55		510 520 530 540 550
	NOV4
	gi 13649119	DRDRMTSVIAVVKNHSLAFVCTKSGKLKKTRVDGPRGNALQYETVQVVD
	gi 3413888	MASVAA YT RQHSVVFIGTRSCSLKKV RVDGFQDAH---LYETV PVV DG
	gi 2134135	MTSVA S VY NG Y SVV FVG TKS C K L K K I RADGP PHGG---V QY EMV S VL K DG
60	gi 14424639	MTSVA AY DY RGHT VV FACTRS CRVKKI LV DLSA SSSHLV QQY EN VV HEG
	gi 10047165	-----
65		560 570 580 590 600
	NOV4
	gi 13649119	PGPFLR DMAFSKDHEQLYIMSERQLTRVPV ESGQYQSCGECLGSGDPHC
	gi 3413888	SPII RDLLFSPDHRH IYI LSEKQVSQLPVETCEQYQSCAACLGSGDPHC
	gi 2134135	SPII RDMAFSIDQRYLYVM SERQVTRVPV ESE QYTTGCECLSSGDPHC
70	gi 14424639	NAI RD LVLSPDRQYIYATEKQVTRVPV ESE QYESCDTCLGSRDPHC
	gi 10047165	-----

			610	620	630	640	650
5	NOV4		GWCVLLENTCTRKBRCRSKPEPFRFASEM[KQCVRLLTVHPPNNISVSQYNVILL				
	gi 13649119		WCVLREHCCREGA[CLGASAPHGFAEELSKCVCVRVRPNNSVTSPGVQIT				
	gi 3413888		WCALHIMCSRRDKCQQAWEPNRF[AA[SI[QCVSLAVHPSSISVEHSRLIS				
	gi 2134135		WCVLHIMCSRKDKCERADELHRFTSDQR[GCVQLTVHKPNLISVTSEVPMV				
10	gi 14424639						
	gi 10047165						
			660	670	680	690	700
15	NOV4		VLETYNVPEL[SAGVNCTFEDLSM[DGLVVGNQI[QCVSEAAKEV[PRLITEN				
	gi 13649119		MLHNVPDLSAGVSCAFEEAAAE[NEAVILPSGEILCPS[SLQEIRALTRGH				
	gi 3413888		L[VVSDAPDLSAGIACAFGNLTEVEGOVS-GS[OVI[ICLSPGPKD[PV[PLDQ				
	gi 2134135		LOAWNVPDL[SAGVNC[SFEDFTEMEGRIL-DGK[IYCTSESAKEV[P[TRGH				
	gi 14424639						
	gi 10047165						
20			710	720	730	740	750
25	NOV4		GDHHV[OLOLKSKETGM[FASTS[FV[FYNC[SVHN[SC[SCVESP[PRCHWCKY				
	gi 13649119		GATRIM[QOLLSKETG[V[R[PAGAD[FV[FYNC[SVLQ[SC[SCVGP[SP[PRCHWCKY				
	gi 3413888		DWFGHELOLRSKETG[KI[PVSTE[FKFYNC[SAHQLC[SC[CVNSA[PRCHWCKY				
	gi 2134135		GD[KRVV[KYLKLSKETG[KKFASVDFEVYNC[SVHQ[SC[SCVNG[SP[PRCHWCKY				
	gi 14424639						
	gi 10047165						
30			760	770	780	790	800
35	NOV4		REV[CIDHPKT[CSFOEQGRV[KVL[EDCPOLI[RVDKIL[PV[EIKP[ITLAKNL				
	gi 13649119		R[ETCTSRPHE[CSFOEQGRV[HSP[EGCP[ELI[PSPGD[L[PVGV[NOP[LTAKNL				
	gi 3413888		RNLCT[DPPT[CSFOEQGRN[IS[EDCP[Q[PTEEL[PVG[EV[KP[ITLAKNL				
	gi 2134135		RHV[CINAAD[CSFOEQGRV[NMSD[DCP[QI[PSSQ[LY[PVG[VK[P[ITLAKNL				
	gi 14424639						
	gi 10047165						
40	NOV4		810	820	830	840	850
	gi 13649119		PQPQSG[QGYEC[LI[NG[SECRVPA[RFN[SSV[Q[CONTSY[SY[FC[MA[INNL				
	gi 3413888		PQPQSG[QKNY[EC[V[VR[QGR[QRP[VA[RFN[SSV[Q[COMAS[SY[SY[CE[DH[GT				
	gi 2134135		PQPQSG[QGYEC[LI[NG[AI[HR[RP[AL[RFN[SSV[Q[CONSSY[QMD[GM[ISNL				
	gi 14424639		PQPQSG[QNY[EC[FH[PG[SV[TR[VT[AL[RFN[ST[SI[Q[CONTSY[SY[EC[NI[DSL				
	gi 10047165						
45			860	870	880	890	900
50	NOV4		P[VELIVVWN[GE[EN[DN[PA[Q[Q[HV[LY[K[CG[AM[RE[CG[GL[CL[K[AD[PD[FA[CG[WC[Q				
	gi 13649119		ELDFSVVWD[G[DE[PD[IKD[KPPS[FL[LY[K[CA[Q[RE[PS[CG[GL[CL[K[AD[PK[PR[NG[GC[WC[Q				
	gi 3413888		AVDFAVVWN[GE[EN[DN[Q[Q[HV[LY[K[CA[Q[RE[PS[CG[GL[CL[K[AD[PK[RE[CG[WC[Q				
	gi 2134135		PVNL[SVVWN[GE[EN[DN[Q[Q[HV[LY[K[CA[Q[RE[PS[CG[GL[CL[K[AD[PK[RE[CG[WC[Q				
	gi 14424639		-VELIVVWN[GE[EN[DN[PA[Q[Q[HV[LY[K[CG[AM[RE[CG[GL[CL[K[AD[PD[FA[CG[WC[Q				
	gi 10047165						
55			910	920	930	940	950
60	NOV4		GPG[CT[LR[QH[CP[Q[OS[Q[Q[HV[LY[K[CG[AM[RE[CG[GL[CL[K[AD[PD[FA[CG[WC[Q				
	gi 13649119		SEH[RC[OL[RT[HC[AP[KT[EN[WH[LS[Q[KT[RC[SH[PR[IT[Q[HV[GP[RE[GG[TR[VT				
	gi 3413888		GERR[CT[LR[QH[CT[SP[SP[Q[Q[HV[LY[K[CG[AM[RE[CG[GL[CL[K[AD[PK[RE[CG[WC[Q				
	gi 2134135		SEKK[CT[LR[QH[CT[EN[PM[HA[ST[AN[SP[Q[KT[PK[KT[Q[FP[ED[PG[RE[GG[TR[VT				
	gi 14424639		GPG[CT[LR[QH[CP[Q[OS[Q[Q[HV[LY[K[CG[AM[RE[CG[GL[CL[K[AD[PD[FA[CG[WC[Q				
	gi 10047165						
65			960	970	980	990	1000
70	NOV4		I[RG[EN[GL[GE[FD[RA[SH[HV[HV[AG[VE[CG[SP[LV[DG[Y[PA[Q[IV[CE[GA-K[PS[Q[Q[HV[
	gi 13649119		I[VG[EN[GL[LS[RE[VG-[LR[VA[CR[CN[SL[PA[BY[IS[AE[RV[CE[ME[ES[SL[VP[SP[PP				
	gi 3413888		I[HV[EN[GL[DE[SP[IA[HH[HV[Q[AG[VG[CP[TL[LP[GE[BY[II[AE[Q[IV[CE[GA-L[VG[TT				
	gi 2134135		I[TC[EN[GL[LR[FE[DI[RF[GV[RV[GH[MC[VP[SE[EV[IS[AE[Q[IV[CE[GA-ND[AG[TR[RV[H				

	gi 14424639	-----				
	gi 10047165	IRGENLGLEFRDIASHVKVAGVECSPIVDGYIPAEOLIVCEMGP-A-KPSQH				
5	NOV4	1010	1020	1030	1040	1050
	gi 13649119	AGFVEITCVAVCREEFMARSSOLYYEMTILSLSDLRPSRGPMGGTQVTITG				
	gi 3413888	PGPVELLCVGDCSADERTQSECVYSEVTPEDQVSPSRGPASCGTRLTISG				
	gi 2134135	SCGPVRICIGECKPEEMTKSHQQYTFVNESVLSTNPIRGPMGGIMVTITG				
10	gi 14424639	EAQVEVCVKDCSODYRAISPKESETVLFPSFNRYTPSRGPLSGGTWISIEG				
	gi 10047165	AGFVEITCVAVCREEFMARSSOLYYEMTILSLSDLRPSRGPMGGTQVTITG				
15	NOV4	1060	1070	1080	1090	1100
	gi 13649119	TNLNAGSNVVMECKOPCPLEHRRSPSYLVCNTSSDE-VLEMKVSVQVDR				
	gi 3413888	SSLDAQSRVITVTRDSECOFVRVDKALVCISPISTLGPSPQPIITIAIDR				
	gi 2134135	HYLCAGSSVAVYLGNOTCEFYGRSMSEIVCVSPSSNGLGPVFVSVSVDR				
20	gi 14424639	NYLNAGSDPSVAAICGRPCOMESWRTAKEIRCKTPQGPS-TGKAETIQLAHN				
	gi 10047165	TNLNAGSNVVMECKOPCPLEHRRSPSYLVCNTSSDE-VLEMKVSVQVDR				
25	NOV4	1110	1120	1130	1140	1150
	gi 13649119	AKITH-ODLVEQVVEDPTIVRIPEPEWSIVSGNTPHAWGTHEDLTONPQIR				
	gi 3413888	ANIISSPGGLIVTYCDPTIVRIPEPEWSIVSGNTPHAWGTHEDLTONPQIR				
	gi 2134135	AHVD-SNLOOEVITDPRVORIEPEPEWSIASCHTPHITITGENLDVIOEPRI				
	gi 14424639	ATMNNSEWYHNNTEDPTVQKIEPEPEWSIASGGTPHITVGMNATIKEPKIR				
30	gi 10047165	AKITH-ODLVEQVVEDPTIVRIPEPEWSIVSGNTPHAWGTHEDLTONPQIR				
35	NOV4	1160	1170	1180	1190	1200
	gi 13649119	AKHGCKEHINICBVLNATEMTQAPALALGPDHQSDLTERPEEEFGFILDN				
	gi 3413888	AKYRCLETTNTCOVENDTAMUCKAPGFLIGRPQPRAQGEHPDEEGFLLDN				
	gi 2134135	VFKFNCKESVNVCAVWNNTTTCCLAPSETTDYRPGLDTVERPDEFGFVFNN				
	gi 14424639	AKYGDVEKEKNNTLYNDTIVCLAPSVDNPLRSPPENCDRPDHTGFIIMDN				
	gi 10047165	-----GTRVVKWVNNTTECTCLAESITTDYRPGLDTVERPDEFGFVFNN				
40	NOV4	1210	1220	1230	1240	1250
	gi 13649119	VQSLLIENKINTFYYPNPVFBAGPSCILELKPCPIILKGKNLIPPPVAG				
	gi 3413888	VQTARSINRNPVYYPDPSPFBLGPSCVLDVKPGSHVVLKGKNLIPPAAG				
	gi 2134135	VQSLLIYNDTKEFYYPNPFTFELLSPICWIKQPGSPIILKGKNLICPPAAG				
	gi 14424639	VHLILIVNTISFVYVPDPVFPPLTASCLKEKPSPLIHKGRNLIPAAAG				
	gi 10047165	VQSLLIYNDTKEFYYPNPFTFELLSPICWIKQPGSPIILKGKNLICPPAAG				
50	NOV4	1260	1270	1280	1290	1300
	gi 13649119	GNVKLNNTVVLVGEKPCTVTSVQOLLCESPNLICRHKVMARVGGMEYSPG				
	gi 3413888	SSPLNNTVVLICQPCSLTVSPQTLQLCSPSOTGRQPVVWAVGCLEWLG				
	gi 2134135	CAKLNNTVVLIGETPCAVTVSETOLLCEBPNLTGCHKVMVWVCGMVFSPG				
	gi 14424639	NFPLNNTVVLIGETPCAVTVSETOLLCEBPNLTGCHKVMVWVCGMVFSPG				
	gi 10047165	GAKLNNTVVLIGETPCAVTVSETOLLCEBPNLTGCHKVMVWVCGMVFSPG				
55	NOV4	1310	1320	1330	1340	1350
	gi 13649119	MVIYIAPDSPISLPAIVSIAVAGGLITIPIVAVLIAVYKRKSRESDLTLKRL				
	gi 3413888	ALHISAAERALTILPAMMGLAAGGLLILIAITAVLIAVYKRKSRESDLTLKRL				
	gi 2134135	SVSVISDSLTLPAIVSIAAGSLLLIVLIVLIAVYKRKSRESDLTLKRL				
	gi 14424639	THQIVSDSLTLPAIIGIGGGGLLILILIVLIAVYKRKSRESDLTLKRL				
60	gi 10047165	SVSVISDSLTLPAIVSIAAGSLLLIVLIVLIAVYKRKSRESDLTLKRL				
65	NOV4	1360	1370	1380	1390	1400
	gi 13649119	MVIYIAPDSPISLPAIVSIAVAGGLITIPIVAVLIAVYKRKSRESDLTLKRL				
	gi 3413888	OMOMDNLESRVALECKEAFELQTDISELTSDDCAGIPFELDYRTYMRV				
	gi 2134135	QFQMDNLESRVALECKEAFELQTDINELTNHMDEVQIPFELDYRTYAVRV				
70						

gi 3413888	QMQMDNLESRVALECKEAFALQTDINELTS	SDLDRS	GIP	YLDYRTYAMRV				
gi 2134135	QMQMDNLESRVALECKEAFALQTDINELT	NLD	CAGIP	YLDYRTYAMRV				
gi 14424639	QMQMDNLESRVALECKEAFALQTDINELT	SDLDRS	GIP	YLDYRTYAMRV				
gi 10047165	QMQMDNLESRVALECKE	G	-	T				
5		1410	1420	1430	1440	1450		
NOV4	LFPGIEDHPVLRELE	VPGYRQER	VEK	KLFAOLINNKV	FLLSFIRTL	ES		
gi 13649119	LFPGIEAH	PVLRELDTPPN	-	VEKA	RLFGOLLESRAF	VLT	FIH	LEA
10	gi 3413888	LFPGIEDHPVLRELE	VQNGQQH	VEKA	KLFAOLINNKV	FLLTFIRTL	EL	
gi 2134135	LFPGIEDHPVLRELE	VQNGQQH	VEKA	KLFAOLINNKV	FLLTFIRTL	EL		
gi 14424639	LFPGIEDHPVLRELE	VQNGQQH	VEKA	KLFAOLINNKV	FLLTFIRTL	EL		
gi 10047165	EWPHAGGH	VQR	-	-	-	-		
15		1460	1470	1480	1490	1500		
NOV4	QRSFSMRDRGNVASLIM	T	VLSKLEYATD	VVLKQLLADLIE	KNLESKNHPK	-		
gi 13649119	QSFSMSMRDRG	T	VASLT	WQSRLDYATG	LLKQLLADLIE	KNLESKNHPK		
20	gi 3413888	QSFSMSMRDRG	NVASLIM	TGLO	RLEYATD	VVLKQLLSDLI	DKNLENKNHPK	
gi 2134135	QSFSMSMRDRG	NVASLIM	TQGEMEYAT	GVLKQLLSDLI	EKNLESKNHPK	-		
gi 14424639	QSFSMSMRDRG	NVASLIM	TGLO	RLEYATD	VVLKQLLSDLI	DKNLENKNHPK		
gi 10047165	-	-	-	-	-	-		
25		1510	1520	1530	1540	1550		
NOV4	LLLRRTESVAEKMLTNWF	T	FLLYKFLKECAGEPLS	S	LFCAIKQQMEKGPI	-		
gi 13649119	LLLRRTESVAEKMLTNWF	T	FLLYKFLKECAGEPL	F	LYCAIKQQMEKGPI	-		
gi 3413888	LLLRRTESVAEKMLTNWF	A	FLLYKFLKECAGEPL	M	LYCAIKQQMEKGPI	-		
gi 2134135	LLLRRTESVAEKMLTNWF	T	FLLYKFLKECAGEPL	M	LYCAIKQQMEKGPI	-		
30	gi 14424639	LLLRRTESVAEKMLTNWF	A	FLLYKFLKECAGEPL	F	LYCAIKQQMEKGPI	-	
gi 10047165	-	-	-	-	-	-		
35		1560	1570	1580	1590	1600		
NOV4	DAITGEARYSLS	SEDKLIRQQIDYKTL	-	-	-	VLS	CV	
gi 13649119	DAITGEARYSLS	SEDKLIRQQIDYKTL	-	-	-	T	LCV	
gi 3413888	DAITGEARYSLS	SEDKLIRQQIDYKTL	-	-	-	I	LNCV	
gi 2134135	DAITGEARYSLS	SEDKLIRQQIDYKTL	-	-	-	I	LNCV	
40	gi 14424639	DAITGEARYSLS	SEDKLIRQQIDYKTL	-	-	-	I	LNCV
gi 10047165	GSAGGWRCV	OLCE	-	-	-	-	CV	
45		1610	1620	1630	1640	1650		
NOV4	SPDNANSPEPV	T	LNCDTTITQVKEK	ILDA	FKVPCSHRPKAADM	DLEW		
gi 13649119	SPDNANSPEPV	KV	VKVLNCDSITQAKDKG	ILDT	VYKGDPVSQRPKAED	MDLEW		
gi 3413888	SPDNANSPEPV	KV	VKVLNCDSITQAKDKG	ILDT	VYKGDPVSQRPKAED	MDLEW		
gi 2134135	SPDNANSPEPV	KV	VKVLNCDSITQAKDKG	ILDT	VYKGDPVSQRPKAED	MDLEW		
gi 14424639	SPDNANSPEPV	KV	VKVLNCDSITQAKDKG	ILDT	VYKGDPVSQRPKAED	MDLEW		
gi 10047165	C	-	-	-	-	-		
50		1660	1670	1680	1690	1700		
NOV4	RQGSCARMILQ	DEDIT	TTTKIENDWKRLNTLIAHYQV	DGSVVALVSKQV	PTAY	-		
gi 13649119	RQGSCARMILQ	DEDIT	TTTKIENDWKRLNTLIAHYQV	DGSVVALVSKQV	PTAY	-		
55	gi 3413888	RQGSCARMILQ	DEDIT	TTTKIENDWKRLNTLIAHYQV	DGSVVALVSKQV	PTAY		
gi 2134135	RQGSCARMILQ	DEDIT	TTTKIENDWKRLNTLIAHYQV	DGSVVALVSKQV	PTAY			
gi 14424639	RQGSCARMILQ	DEDIT	TTTKIENDWKRLNTLIAHYQV	DGSVVALVSKQV	PTAY			
gi 10047165	RQGSCARMILQ	DEDIT	TTTKIENDWKRLNTLIAHYQV	DGSVVALVSKQV	PTAY			
60		1710	1720	1730	1740	1750		
NOV4	NAVNNSTVS	RTISASKYENMI	RTGSPDSLRSRT	PMITPD	LESCV	IKWHLV		
gi 13649119	NMANSEMP	RTISASKYENMI	RTGSPDSLRSRT	PMITPD	QETG	IKWHLV		
gi 3413888	NPASASISR	ISASISR	RTGSPDSLRSRT	PMITPD	QETG	IKWHLV		
65	gi 2134135	NPASASISR	ISASISR	RTGSPDSLRSRT	PMITPD	QETG	IKWHLV	
gi 14424639	NPASASISR	ISASISR	RTGSPDSLRSRT	PMITPD	QETG	IKWHLV		
gi 10047165	NPASASISR	ISASISR	RTGSPDSLRSRT	PMITPD	QETG	IKWHLV		
70		1760	1770	1780	1790	1800		

	NOV4	KNHEDCDCKEGDRGSKMVSIEYLTRLLATKGTLQKFVDDLFEIIFSTAHR
5	gi 13649119	KNHHDADHREGDRGSKMVSIEYLTRLLATKGTLQKFVDDLFEIIFSTAHR
	gi 3413888	KNHHDADHREGDRGSKMVSIEYLTRLLATKGTLQKFVDDLFEIIFSTAHR
	gi 2134135	KNHHDADHREGDRGSKMVSIEYLTRLLATKGTLQKFVDDLFEIIFSTAHR
	gi 14424639	KNHHDADHREGDRGSKMVSIEYLTRLLATKGTLQKFVDDLFEIIFSTAHR
	gi 10047165	KNHHDADHREGDRGSKMVSIEYLTRLLATKGTLQKFVDDLFEIIFSTAHR
		1810 1820 1830 1840 1850
10	NOV4	GSALPLAIKYMFDLDEQADRHGIHDVVRHRTWSNCLPLRFWVNVIKNP
	gi 13649119	GSALPLAIKYMFDLDEQADRHQSIDHDVVRHRTWSNCLPLRFWVNVIKNP
	gi 3413888	GSALPLAIKYMFDLDEQADRHQSIDHDVVRHRTWSNCLPLRFWVNVIKNP
	gi 2134135	GSALPLAIKYMFDLDEQADRHQSIDHDVVRHRTWSNCLPLRFWVNVIKNP
	gi 14424639	GSALPLAIKYMFDLDEQADRHQSIDHDVVRHRTWSNCLPLRFWVNVIKNP
	gi 10047165	GSALPLAIKYMFDLDEQADRHQSIDHDVVRHRTWSNCLPLRFWVNVIKNP
		1860 1870 1880 1890 1900
15	NOV4	QFVFDIHKSITDACLSSVVAQTFMDSCSTSEHRLGKDSPSNKLLYAKDIP
	gi 13649119	QFVFDIHKSITDACLSSVVAQTFMDSCSTSEHRLGKDSPSNKLLYAKDIP
	gi 3413888	QFVFDIHKSITDACLSSVVAQTFMDSCSTSEHRLGKDSPSNKLLYAKDIP
	gi 2134135	QFVFDIHKSITDACLSSVVAQTFMDSCSTSEHRLGKDSPSNKLLYAKDIP
	gi 14424639	QFVFDIHKSITDACLSSVVAQTFMDSCSTSEHRLGKDSPSNKLLYAKDIP
	gi 10047165	QFVFDIHKSITDACLSSVVAQTFMDSCSTSEHRLGKDSPSNKLLYAKDIP
		1910 1920 1930 1940 1950
20	NOV4	SYKSWVERYYSDICKNPVISQDQDMAYLAEQSRHINNEFNIVSALISE-ES
	gi 13649119	NYKSWSVERYYRDIAKMAISQDQDMAYLVEQSRHLASDFSVLSALNEIYS
	gi 3413888	SYKSWVERYYRDIAKMAISQDQDMAYLVEQSRHLASDFSVLSALNEIYS
	gi 2134135	NYKSWSVERYYRDIAKMAISQDQDMAYLVEQSRHLASDFSVLSALNEIYS
	gi 14424639	SYKSWVERYYRDIAKMAISQDQDMAYLVEQSRHLASDFSVLSALNEIYS
	gi 10047165	SYKSWVERYYRDIAKMAISQDQDMAYLVEQSRHLASDFSVLSALNEIYS
		1960 1970 1980 1990
25	NOV4	YVCKYSEPIILCPILDQCGKOKLAVKPQEQQVITLMSLDNSK
	gi 13649119	YVTKYRQEPIILTALDRDASCRKHLROKDEQIIISLVSSDS--
	gi 3413888	YVSKYSEBDIGALEQDEOARORLAYKEQLINAMSIES--
	gi 2134135	YVSKYRQEPIILTALDRDARORLRSKQEVIDITWMOSS--
	gi 14424639	YVSKYSEBDIGALEQDEOARORLAYKEQLINAMSIES--
	gi 10047165	YVSKYSEBDIGALEQDEOARORLAYKEQLINAMSIES--

45 Tables 4E-K list the domain description from DOMAIN analysis results against
NOV4. This indicates that the NOV4 sequence has properties similar to those of other
proteins known to contain this domain.

Table 4E. Domain Analysis of NOV4

gnl|Smart|smart00630, Sema, semaphorin domain (SEQ ID NO:76)
CD-Length = 430 residues, 100.0% aligned
Score = 226 bits (575), Expect = 1e-59

Table 4F. Domain Analysis of NOV4

gml|Pfam|pfam01403, Sema, Sema domain. The Sema domain occurs in semaphorins, which are a large family of secreted and transmembrane proteins, some of which function as repellent signals during axon guidance. Sema domains also occur in the hepatocyte growth factor receptor. (SEQ ID NO:77)
CD-Length = 433 residues, 100.0% aligned
Score = 186 bits (471). Expect = 1e-47

Table 4G. Domain Analysis of NOV4

gnl|Pfam|pfam01833, TIG, IPT/TIG domain. This family consists of a domain that has an immunoglobulin like fold. These domains are found in cell surface receptors such as Met and Ron as well as in intracellular transcription factors where it is involved in DNA binding. CAUTION: This family does not currently recognise a significant number of members. (SEQ ID NO:78)
CD-Length = 85 residues, 98.8% aligned
Score = 69.7 bits (169), Expect = 1e-12

Query:	955	TLSDLKPSSRGPMSSGGTQVTTGTNLNAGSNVVVMFGKQPCFHRRSPSYIVCMTTSSDEV	1014
		++ + + + + + + + +	
Sbjct:	2	VITSISPPSGPLSGGTETITIGSNLGSQEDIKVTGGTECDVVSQEASQIVCKTPPYANG	61
Query:	1015	LEMKVSVQVDRA-KIHQDLVFTQYV	1037
		+ + +	
Sbjct:	62	GPQPVTVSLDGGLSSPVTFTYV	85

Table 4H. Domain Analysis of NOV4

gnl|Pfam|pfam01833, TIG, IPT/TIG domain. This family consists of a domain that has an immunoglobulin like fold. These domains are found in cell surface receptors such as Met and Ron as well as in intracellular transcription factors where it is involved in DNA binding. CAUTION: This family does not currently recognise a significant number of members. (SEQ ID NO.79)
CD-Length = 85 residues, 91.8% aligned
Score = 54.3 bits (129), Expect = 6e-08

Table 4I. Domain Analysis of NOV4

gnl|pfam|pfam01833, TIG, IPT/TIG domain. This family consists of a domain that has an immunoglobulin like fold. These domains are found in cell surface receptors such as Met and Ron as well as in intracellular transcription factors where it is involved in DNA binding. CAUTION: This family does not currently recognise a significant number of members. (SEQ ID NO:80)
CD-Length = 85 residues, 100.0% aligned
Score = 45.8 bits (107), Expect = 2e-05

Query: 1040 PTIVRIEPEWSIVSGNTPIAVWGTHLDLIQNPQIRAKHGGKEHINICEVNL--ATEMTCQ 1097
 | | | | + | | | + |++| ++ |+ | | | | + |++| + |++| + |+|
 25 Sbjct: 1 PVITSISPSSGPGPLSGGTEITITGSNLGSGED--IKVTFGGT-----CDVVSOEAROIVCK 54

Query: 1098 APALALGPDHQSDLTERPEEFGFILDNVQSLLLNLNKTNFYY 1139
 | | + || | + || | + ||
 Sbjct: 55 TPPYA-----NGGPQPVTVSLDGGG--LSSSPVTFTYV 85

5

Table 4J Domain Analysis of NOV4

gnl|Smart|smart00423, PSI, domain found in Plexins, Semaphorins and Integrins (SEQ ID NO:81)
 CD-Length = 47 residues, 100.0% aligned
 Score = 46.6 bits (109), Expect = 1e-05

Query: 655 NCSVHNSCLSCVESPYR-CHWCKYRHVCTHDPKTCFSQEGRVKLPEDCP 702
 || + || | + + | | + || | + || | || |
 Sbjct: 1 RCSAYTSCSECLLARDPYCAWCSSQGRCTSGB-RCDSLRQNW-SSGQCP 47

Table 4K. Domain Analysis of NOV4

gnl|Smart|smart00429, IPT, Ig-like, plexins, transcription factors (SEQ ID NO:82)
 CD-Length = 93 residues, 100.0% aligned
 Score = 57.8 bits (138), Expect = 6e-09

Query: 1039 DPTIVRIEPEWSIVSGNTPIAVWGTHLDDLIQNPQIRAKHGGKEHINICEVLNATEMTCQA 1098
 || | | | | + || | | + | + || | + | + ++ | + | + | +
 Sbjct: 1 DPVITRISPNSGPLSGGTRITLCGKNLDISVVVFVEVGVGEVPCTFLPSDVSQTAIVCKT 60

Query: 1099 PALALGPDHQSDLTERPEEFGFILDNVQSLLLNLNKTNFYY 1139
 | | | | | | | + || |
 Sbjct: 61 PPYHNTP----GSVPVRVEVGLRNNGVPGE---PSPFTYV 93

Semaphorins are a large family of secreted or cell-bound signals, known to guide axons in developing nervous tissue. They are expressed in a variety of adult and embryonic tissues and are thought to have a broader spectrum of functions. Recent evidence suggests that semaphorins and their receptors play a key role in the control of cellular interactions, most likely in cell-cell repulsion (Tamagnone and Comoglio. Trends Cell Biol 2000 Sep;10(9):377-83.). A subset of semaphorins interacts with neuropilins - cell-surface molecules lacking a signalling-competent cytoplasmic domain. Another large family of transmembrane molecules, namely plexins, bind specifically to semaphorins. Thus plexins, alone, or in association with neuropilins, behave as fully functional semaphorin receptors. The intracellular responses elicited by plexins are unknown, but their large cytoplasmic moiety, containing the strikingly conserved sex-plexin (SP) domain, is likely to trigger novel signal-transduction pathways.

Chemorepulsive signals such as the semaphorins play an essential role in navigating axons over large distances in the developing nervous system. The effects of one of these repulsive cues, semaphorin 3A (Sema3A), are mediated by the membrane protein neuropilin-1 (Npn-1). Recent work has shown that neuropilin-1 is essential but not sufficient to form functional Sema3A receptors and indicates that additional components are required to transduce signals from the cell surface to the cytoskeleton (Rohm et al. *Mech Dev* 2000 May;93(1-2):95-104). It has been shown that members of the plexin family interact with the neuropilins and act as co-receptors for Sema3A. Neuropilin/plexin interaction restricts the binding specificity of neuropilin-1 and allows the receptor complex to discriminate between two different semaphorins. Deletion of the highly conserved cytoplasmic domain of Plexin-A1 or -A2 creates a dominant negative Sema3A receptor that renders sensory axons resistant to the repulsive effects of Sema3A when expressed in sensory ganglia. These data suggest that functional semaphorin receptors contain plexins as signal-transducing and neuropilins as ligand-binding subunits.

Class 1 and 3 semaphorins repulse axons but bind to different cell surface proteins. Two known semaphorin-binding proteins, plexin 1 (Plex 1) and neuropilin-1 (NP-1), form a stable complex (Strittmatter. *Cell* 1999 Oct 1;99(1):59-69.). Plex 1 alone does not bind semaphorin-3A (Sema3A), but the NP-1/Plex 1 complex has a higher affinity for Sema3A than does NP-1 alone. While Sema3A binding to NP-1 does not alter nonneuronal cell morphology, Sema3A interaction with NP-1/Plex 1 complexes induces adherent cells to round up. Expression of a dominant-negative Plex 1 in sensory neurons blocks Sema3A-induced growth cone collapse. Sema3A treatment leads to the redistribution of growth cone NP-1 and plexin into clusters. Thus, physiologic Sema3A receptors consist of NP-1/plexin complexes.

As mentioned previously, the semaphorin family of molecules contains members known to deliver guidance cues to migrating axons during development. Semaphorins also have been identified on the surface of hematopoietic cells and, interestingly, in the genomes of certain lytic viruses. Recent studies indicate that semaphorins bind with high affinity to at least two different receptor families and are biologically active on immune cells as well as neuronal cells (Spriggs. *Curr Opin Immunol* 1999 Aug;11(4):387-91.).

The mammalian olfactory system is capable of discriminating among a large variety of odor molecules and is therefore essential for the identification of food, enemies and mating partners. The assembly and maintenance of olfactory connectivity have been shown to depend on the combinatorial actions of a variety of molecular signals, including extracellular matrix, cell adhesion and odorant receptor molecules (Pasterkamp et al. *Cell Mol Biol* 1999

Sep;45(6):763-79). Recent studies have identified semaphorins and their receptors as putative molecular cues involved in olfactory pathfinding, plasticity and regeneration. Neuropilins were shown to serve as receptors for secreted class 3 semaphorins, whereas members of the plexin family are receptors for class 1 and V (viral) semaphorins.

5 In *Drosophila*, plexin A is a functional receptor for semaphorin-1a. The human plexin gene family comprises at least nine members in four subfamilies (Goodman et al. Cell 1999 Oct 1;99(1):71-80.). Plexin-B1 is a receptor for the transmembrane semaphorin Sema4D (CD100), and plexin-C1 is a receptor for the GPI-anchored semaphorin Sema7A (Sema-K1). Secreted (class 3) semaphorins do not bind directly to plexins, but rather plexins associate with 10 neuropilins, coreceptors for these semaphorins. Plexins are widely expressed: in neurons, the expression of a truncated plexin-A1 protein blocks axon repulsion by Sema3A. The cytoplasmic domain of plexins associates with a tyrosine kinase activity. Plexins may also act as ligands mediating repulsion in epithelial cells in vitro. Plexins are receptors for multiple (and perhaps all) classes of semaphorins, either alone or in combination with neuropilins, and 15 trigger a novel signal transduction pathway controlling cell repulsion.

Plexin is a type I membrane protein which was identified in *Xenopus* nervous system by hybridoma technique. Molecular cloning studies demonstrated that the extracellular segment of the plexin protein possesses three internal repeats of cysteine cluster which are homologous to the cysteine-rich domain of the c-met proto-oncogene protein product. A cell 20 aggregation test revealed that the plexin protein mediated cell adhesion via a homophilic binding mechanism, in the presence of calcium ions (Fujisawa et al. Dev Neurosci 1997;19(1):101-5.). Plexin was expressed in the neuronal elements composing particular neuron circuits in *Xenopus* CNS and PNS. These findings indicate that plexin is a new member of the Ca(2+)-dependent cell adhesion molecules, and suggest that the molecule plays 25 an important role in neuronal cell contact and neuron network formation.

Plexin (previously referred to as B2) is a neuronal cell surface molecule that has been identified in *Xenopus*. cDNA cloning reveals that plexin has no homology to known neuronal cell surface molecules but possesses, in its extracellular segment, three internal repeats of cysteine clusters that are homologous to the cysteine-rich domain of the c-met proto-oncogene 30 protein product. The exogenous plexin proteins expressed on the surfaces of L cells by cDNA transfection mediate cell adhesion via a homophilic binding mechanism, under the presence of calcium ions (Fujisawa. Neuron 1995 Jun;14(6):1189-99.). Plexin is expressed in the receptors and neurons of particular sensory systems. These findings indicate that plexin is a

novel calcium-dependent cell adhesion molecule and suggest its involvement in specific neuronal cell interaction and/or contact.

The disclosed NOV4 nucleic acid of the invention encoding a Plexin -like protein includes the nucleic acid whose sequence is provided in Table 4A or a fragment thereof. The 5 invention also includes a mutant or variant nucleic acid any of whose bases may be changed from the corresponding base shown in Table 4A while still encoding a protein that maintains its Plexin -like activities and physiological functions, or a fragment of such a nucleic acid. The invention further includes nucleic acids whose sequences are complementary to those just described, including nucleic acid fragments that are complementary to any of the nucleic acids 10 just described. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications. Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be 15 used, for example, as antisense binding nucleic acids in therapeutic applications in a subject. In the mutant or variant nucleic acids, and their complements, up to about 29% percent of the bases may be so changed.

The disclosed NOV4 protein of the invention includes the Plexin -like protein whose sequence is provided in Table 4B. The invention also includes a mutant or variant protein any 20 of whose residues may be changed from the corresponding residue shown in Table 4B while still encoding a protein that maintains its Plexin -like activities and physiological functions, or a functional fragment thereof. In the mutant or variant protein, up to about 40% percent of the residues may be so changed.

The protein similarity information, expression pattern, and map location for the Plexin-like protein and nucleic acid (NOV4) disclosed herein suggest that this NOV4 protein may 25 have important structural and/or physiological functions characteristic of the Plexin family. Therefore, the NOV4 nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications. These include serving as a specific or selective nucleic acid or protein diagnostic and/or prognostic marker, wherein the presence or amount 30 of the nucleic acid or the protein are to be assessed, as well as potential therapeutic applications such as the following: (i) a protein therapeutic, (ii) a small molecule drug target, (iii) an antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) a nucleic acid useful in gene therapy (gene delivery/gene ablation), and (v) a composition promoting tissue regeneration in vitro and in vivo.

The NOV4 nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications implicated in various diseases and disorders described below. For example, the compositions of the present invention will have efficacy for treatment of patients suffering from Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neurodegeneration, Systemic lupus erythematosus, Autoimmune disease, Asthma, Emphysema, Scleroderma, allergy, ARDS, Obesity, Metabolic Dysregulation, Infertility, and/or other pathologies. The NOV4 nucleic acids, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

NOV4 nucleic acids and polypeptides are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-NOVX Antibodies" section below. For example, the disclosed NOV4 protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated NOV4 epitope is from about amino acids 20 to 30. In another embodiment, a NOV4 epitope is from about amino acids 180 to 190. In additional embodiments, NOV4 epitopes are from about amino acids 180 to 270, from about amino acids 310 to 320, from about amino acids 380 to 390, from about amino acids 400 to 405, from about amino acids 420 to 550, from about amino acids 620 to 630, from about amino acids 650 to 700, from about amino acids 790 to 900, from about amino acids 1040 to 1050, from about amino acids 1100 to 1120, from about amino acids 1220 to 1240, from about amino acids 1410 to 1420, from about amino acids 1450 to 1500, from about amino acids 1580 to 1600, from about amino acids 1620 to 1650, from about amino acids 1720 to 1730 and from about amino acids 1800 to 1900. These novel proteins can be used in assay systems for functional analysis of various human disorders, which will help in understanding of pathology of the disease and development of new drug targets for various disorders.

30

NOV5

A disclosed NOV5 nucleic acid of 1535 nucleotides (also referred to as GMAC027612_A) encoding a novel dopamine receptor-like protein is shown in Table 5A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 7-9

and ending with a TAA codon at nucleotides 1447-1449. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 5A, and the start and stop codons are in bold letters.

Table 5A. NOV5 Nucleotide Sequence (SEQ ID NO:14)

```

CCCGAAATGCTGCCGCAAGGAGCAACGACACCGCGTACCGGGCAGTTAGCGCTATACCA
GCAGCTGGCGCAGGGGAATGCCGTGGGGGCTGGCGGGGGCACGCCACTGGGCCCCGTGC
AGGTGGTCACCGCCTGCTGCTGACCCCTACTCGTCATCTGGACCTTGCTGGCAACGTCTG
GTGTCAGGCCATCTGTGGACCCGCCACTTGCAGCGCAAGAGTACCAACGCTTCATTGT
GTCTCTACCTGTGTCAGACCTCTTGTGGCTGGCTGGTGTGGAAAGGCAGTCGCCG
AGGTGGCGGTTACTGGCCCTTGAAGCGTTCTGCGACGTGGTGGCCTTCGACATCATG
TGCTCCACCCCTCCATCTGAACCTGTGCGTCATCAGCGTGGCCGCTACTGGGCCATCTC
CAGGCCCTTCGCTACGAGCGCAAGATGACCAGCGCATGGCCTGGTCATGGTCCGCCGG
CCTGGACCTTGTCCAGCCTCATCTCTTCAATTCCGGTCCAGCTCAACTGGCACAGGGACCCAG
GGGGTCTCTGGGGGGCTGGGCTGGACCTGCCAACACCTGGCCAATGGACGCCCTGGGAGGA
GGCGTTGGGAGCCGACGTGGAGAGAACTGTGACTCCAGCTGAATCGAACCTACG
CCATCCCCTCTCGTCATCAGCTCTACATCCCATEGCCATCATGATCGTGAACCTACAG
CGCATCTACCGCATCCCCCAGGTGAGATCCGAGGATTCTCCCTGGAGAGGGCCGAGA
GCACGTGAGAGCTGCCGGAGCAGCGCAGGCTGCACGCCGACACCAGCCCTGGGTTTCCA
TCAAGAAGGAGACCGGGTTCTCAAGACCCCTGCGGTGATCATGGGGTCTTCGTTGTTGC
TGGCTGCCCTCTTCATCTTAACITGATGGTTCTTCGAGTGGACACCCCCAAGGCC
TCCGGCCGGCTTCCCTGCGTCAGTAGAGACCAATTGATGTCTTCATCTGGTCTGGG
CCAACCTCTACTCAACCCAGTCCCCAGTCACTATGCCCTCAACGCCACTCCGGAGGTG
TTTGGCCAGCTGCTGGGGTGCAGCACGTCTGCCCGCACGCCGGAGACGGTGAACAT
CAGCAATGAGCTCATCTCTCAACCCAAGACACGGCTTCCACAGGAATCCAGCTGCC
ACATCCACATGCCCCAGGCCATCCCCCGGGACCGGGAGGGTGAACACGATGAGGAG
GAGGAGAGCTCTGCTGGAGCTGGACTGCGAGGGGGAGATTCTTAGACAAAAAAACACCTT
TCACCCCAAATGGATTCCATTAAACTGCAATTAGAAACCCCTCATGGATCTGCATAACCAC
ACAGACATTGACAAGCATGCACACACAAGCAAATACATGGCTTCCA

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5

The NOV5 nucleic acid was identified on chromosome 4 and has 1494 of 1536 bases (97%) identical to a Human dopamine receptor (D5) transcribed pseudogene mRNA from *Homo sapiens* (GENBANK-ID: M75867) (E = 0.0)

- A disclosed NOV5 polypeptide (SEQ ID NO:15) encoded by SEQ ID NO:14 is 480 amino acid residues and is presented using the one-letter code in Table 5B. Signal P, Psort and/or Hydropathy results predict that NOV5 has a signal peptide and is likely to be localized in the plasma membrane with a certainty of 0.6400. In other embodiments, NOV5 may also be localized to the Golgi body with acertainty of 0.4600, the endoplasmic reticulum (membrane) with a certainty of 0.3700, or the endoplasmic reticulum (lumen) with a certainty of 0.1000.
- 15 The most likely cleavage site for a NOV5 peptide is between amino acids 63 and 64, at: VSA-AI.

Table 5B. Encoded NOV5 protein sequence (SEQ ID NO:15)

```

MLPPRSNDTAYPGQLALYQQLAQGNAVGGSAGAPPLGPVQVVTACLLTLVIWLLGNVLVSAAIWWSRHLR
AKMTNVFTIVSLPVSDLFVALLVMSWKAVAEVAGYWPPEAFCDVVWAFDIMCSTASILNLCVISVARYWAISR
PFRYERKMTORMALVMVRPAWTLSLISFIPVQLNWHRDQAVSWGGLDPNNLANWTPWEAVWEPDVRAEN

```

CDSSLNRTYAIPSSLISFYIPMAIMIVTYTRIYRIAQVQIRRSSLERAEEHVOSCRSSAGCTPDTSLRFSI
 KKTEEVLKTLVIMGVFVCCWLPPFILNCMVPFCGHPKGPPAGFPVCSETTFDVFIFWFCWANSSLNPVPSH
 YAFNADFRKVFAQLLGCSHVCSTRPVETVNISNELISYNQDTVFKEIAAAAYIHMMMPNAIPPGDREVDNDEE
 EESPFDMSQIYQTSPGDHVAESVWELDCGEGLSLDKITPFPTPNGFH

The disclosed NOV5 amino acid sequence has 437 of 480 amino acid residues (91%) identical to, and 446 of 480 amino acid residues (92%) similar to, the 477 amino acid residue DOPAMINE RECEPTOR (D(5) DOPAMINE RECEPTOR) (D1BETA DOPAMINE RECEPTOR) protein from *Homo sapiens* (Human) (P21918) ($E = 3.3e^{-237}$).

NOV5 is expressed in at least the following tissues: fetal heart, pooled human melanocyte, fetal heart, and pregnant uterus. TaqMan data for NOV5 is shown below in Example 2.

NOV5 also has homology to the amino acid sequences shown in the BLASTP data listed in Table 5C.

Table 5C. BLAST results for NOV5					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 4503391 ref NP_00789.1	dopamine receptor D5; Dopamine receptor D1B [Homo sapiens]	477	437/480 (91%)	446/480 (92%)	0.0
gi 6978781 ref NP_036900.1	D(1B) DOPAMINE RECEPTOR (D(5) DOPAMINE RECEPTOR)	475	376/480 (78%)	403/480 (83%)	0.0
gi 1169230 sp P42290 DBDR_XENLA	D(1B) DOPAMINE RECEPTOR (D(5) DOPAMINE RECEPTOR)	457	299/445 (67%)	341/445 (76%)	e-158
gi 1362719 pir B55886	dopamine receptor D1B - chicken	486	321/483 (66%)	353/483 (72%)	e-157
gi 1518040 gb AAC60070.1	dopamine D1B receptor [Anguilla anguilla]	458	297/446 (66%)	346/446 (76%)	e-154

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 5D.

Table 5D Clustal W Sequence Alignment

- 1) NOV5 (SEQ ID NO:15)
- 2) gi|4503391|ref|NP_00789.1| dopamine receptor D5; Dopamine receptor D1B [Homo sapiens] (SEQ ID NO:47)
- 3) gi|6978781|ref|NP_036900.1| D(1B) DOPAMINE RECEPTOR (D(5) DOPAMINE RECEPTOR) (SEQ ID NO:48)
- 4) gi|1169230|sp|P42290|DBDR_XENLA D(1B) DOPAMINE RECEPTOR (D(5) DOPAMINE RECEPTOR) (SEQ ID NO:49)
- 5) gi|1362719|pir||B55886 dopamine receptor D1B - chicken (SEQ ID NO:50)
- 20 6) gi|1518040|gb|AAC60070.1| dopamine D1B receptor [Anguilla anguilla] (SEQ ID NO:51)

	10	20	30	40	50	
5	NOV5 gi 4503391 gi 6978781 gi 1169230 gi 1362719 gi 1518040	MLPPRSNDTAYP-CQIALYQQQLAQGNAVCGSAGAPPLG--PVQVVTACLL MLPPGSNGHAYP-CQFALYQQQLAQGNAVCGSAGAPPLG--PSQVVTACLL MLPPGRNRTAQP-AFLGLQRQLAQVDAPLGA-TPLG--PAQVVTAGLL MYOPFQHIDS--DQVASWQSPEMLMNKSVSRESQRKELVAGOIVTGSLL -----MLRG---CRSPLPPP--AGPPCGARGQAGAG-AAQVAAGSLL MGSPAKYLSVHETQSVPFFIGEIMWNTSEAEKTDGKELIVFTVGCLL				
10		60	70	80	90	100
15	NOV5 gi 4503391 gi 6978781 gi 1169230 gi 1362719 gi 1518040	TLLVIWTLLGNVLVSAAIIVSRHLRAKTMVFIIVSLPVSSDLFVALLVMsw TLLLIWTLLGNVLVCAAIIVRSRHLRANMTMVFIIVSLAVSDLFVALLVMPw TLLIWTLLGNVLVCAAIIVRSRHLRAKTMNIFIVSLAVSDLFVALLVMPw LLLIEWTLFGNLIVCCTAVMRFRHLRSRVNIFIVSLAVSDLFVALLVMPw ALLIEWTLFGNVLVCAAIIVRVMRHLRSKVTNIFIVSLAVSDLFVAVLVMPw SLLIWTLLGNLIVCSAVLKFRHLRTKUTNIFIVSLAVSDLFVAVLVMPw				
20		110	120	130	140	150
25	NOV5 gi 4503391 gi 6978781 gi 1169230 gi 1362719 gi 1518040	KAVAEVAGYWPFBAFCDVWVAFDIMCSTASILNLCVISVARYWAISRPFR KAVAEVAGYWPFGAFCDVWVAFDIMCSTASILNLCVISVDRYWAISRPFR KAVAEVAGYWFCDFCDIVWVAFDIMCSTASILNLCVISVDRYWAISRPFR KAVAEVAGHWPPGAFCDIVWVAFDIMCSTASILNLCVISVDRYWAISSPFR KAVAEVAGYWPPGAFQNVWVAFDIMCSTASILNLCVISVDRYWAISSPFR KAVAEVAGYWPFGBFCNIVWVAFDIMCSTASILNLCVISVDRYWAISSPFR				
30		160	170	180	190	200
35	NOV5 gi 4503391 gi 6978781 gi 1169230 gi 1362719 gi 1518040	YERKMTQRMALVMVRPAWTLSLISFIPVQLNWHRDQAVSWGG---L-- YERKMTORMALVMVGLAWTLSLISFIPVQLNWHRDQAAASWGG---L-- YERKMTQRVALVMVGLAWTLSLISFIPVQLNWHRDQAGSQ---L-- YERKMTQRVALMISTAWALSVLISFIPVQLWSHE---L-- YERKMTQRVALVMVGVAVALSVLISFIPVQLNWHRGGDAATAAAAGDIED YERKMTQRVALVMNSVWTLSLISFIPVQLNWHEKAS---				
40		210	220	230	240	250
45	NOV5 gi 4503391 gi 6978781 gi 1169230 gi 1362719 gi 1518040	-----D-----LPNNILANWDPWEAVWEWP -----D-----LPNNILANWDPWEFPFWEPD -----QEGILSNGTDPMEPG-WELE -----TEDHILLSNHSTG----- GFDTGWEAAGAFTTWAEDMSTTWVALAAMTPSEGTSGNNNTVPCP----- -----DEBWINNGFEGCEK-----				
50		260	270	280	290	300
55	NOV5 gi 4503391 gi 6978781 gi 1169230 gi 1362719 gi 1518040	VPAENCDSSLNRTYTAIPSSLISFYIPVAIMIVTYTRIYRIAQVOIRRIS VNAENCDSSLNRTYTAISSSLISFYIPVAIMIVTYTRIYRIAQVOIRRIS GRLENCDSSLNRTYTAISSSLISFYIPVAIMIVTYTRIYRIAQVOIRRIS ---NCDSSLNRTYTAISSSLISFYIPVAIMIVTYTRIYRIAQVOIRRIS ---SESCDSSLNRTYTAISSSLISFYIPVAIMIVTYTRIYRIAQVOIRRIS ---SENCDSSLNRTYTAISSSLISFYIPVAIMIVTYTRIYRIAQVOIRRIS				
60		310	320	330	340	350
65	NOV5 gi 4503391 gi 6978781 gi 1169230 gi 1362719 gi 1518040	LERAEEHVQCSRSGACT---PDTSLRFSIKKETEVLKTLTSVIMGVFVC LERAEEHAQCSRSSAAC---PDTSLRASIKKETKVLKTLTSVIMGVFVC LERAEEHAQCSRSGRAYE---PDTSLRASIKKETKVKTLTSVIMGVFVC LERAEEHAQCSRNRVDSCSRHHQTSLIRTSIKKETKVLKTLTSVIMGVFVC LERAEEHAQCSRCHVDC---HHHTSLRKSIRKETKVLKTLTSVIMGVFVC LERAEEHAQCSRNRLEC---QHHNTLTSIKRKTKEVFKTLTSVIMGVFVC				
70		360	370	380	390	400
	NOV5 gi 4503391 gi 6978781 gi 1169230 gi 1362719	CWLPPFFILNCMVPFCG-GHEKGPPAGFPCVSETTFDVFIFWFGWANSSLNP CWLPPFFILNCMVPFCG-GHEEGPPAGFPCVSETTFDVFIFWFGWANSSLNP CWLPPFFILNCMVPFCGSSCDAEGPKTGEPFPCVSETTFDIFVWFGWANSSLNP CWLPPFFILNCMVPFCG-RSFQAGLPCVSETTFDIFVWFGWANSSLNP CWLPPFFILNCMVPFCG-SPPSDPRAGLPCVSETTFNIFVWFGWANSSLNP				

gi 1518040]	CWLPFFILNCIVPFCD-RPPTDHTAGLPCVSDTTFDVFVWFGLNTSSLNPK
	410 420 430 440 450
5 NOVS	WPSHAYAFNAFDRKVFQALLGCSHIVCSCPVPETVNISNELLISYNQDTIFHK
gi 4503391	M--IYAFNAFDQKVFAQLLGCSCSHFCSCPVPETVNISNELLISYNQDTIFHK
gi 6978781	I--IYAFNAFDRKVFQALLGCSHFCRIPVQTVNISNELLISYNQDTIFHK
gi 1169230	I--IYAFNAFDRKVFESSLLGCQGHWCSTTPVETVNISNELLISYNQDTIFHK
gi 1362719	I--IYAFNAFDRKVFESNLIGCGQFCSCPVPETVNISNELLISYHQDTIFHK
10 gi 1518040	I--IYAFNAFDRKAFAQLLGCRNFCSCPVPETVNISNELLISYNQDTIFHK
	460 470 480 490 500
15 NOVS	EIAAAAYTENMENAIIPPGCDREVNDNDEEESPFDRMSQIQYQISPDPGDHVAAES
gi 4503391	EIAAAAYTENMMPNAAVTPGNNREVNDNDEE-CPFDRMFQIQYQISPDPGDHVAAES
gi 6978781	EIAATAYVEMIPNAVSSGDRREVGEHEEE-CPFDEMSQISISETTPDGDAAES
gi 1169230	DEVITAYVNMIPNVV-----DCIDPDNE-AFDHMSQISQISIANNEELATDS
gi 1362719	EVVTAYVNMIPNVV-----DCCEENRSQ-PFDRMSQISISP---DPSEVATDS
20 gi 1518040	EVITAYVNMIPNVV-----DCIDPDNE-TFDRISQFSH---NNELATDS
	510 520
NOVS	VWELDC-BCEISLDKITPFTPNGFB---
25 gi 4503391	VWELDC-BCEISLDKITPFTPNGFB---
gi 6978781	VWELDC-BCEISLDKITPFTPNGFB---
gi 1169230	VCELDS-BVDISLKEITPSMSNCI---
gi 1362719	VCELDC-BCEISLDKITPFTPNGFB---
gi 1518040	VCDLDDCBAICLDPRIAPFTPNGFB---

30 Tables 5E list the domain description from DOMAIN analysis results against NOV5.
This indicates that the NOV5 sequence has properties similar to those of other proteins known
to contain this domain.

Table 5E. Domain Analysis of NOV5

gml|Pfam|pfam00001, 7tm_1, 7 transmembrane receptor (rhodopsin family). (SEQ ID NO:83)
CD-Length = 254 residues, 99.2% aligned
Score = 188 bits (478), Expect = 5e-49

35	Query:	57	GNNVLVSAAIIVWSRHLRAKMTNVFIVSLPVSDFLVALLVMSWKAVAEVAGYWPF-EAFCDV + + ++ + +++ + + + +	115
	Sbjct:	1	GNLLVLVILVLRTKKL-R-TPTNIFLNLAVADLLFLTLPPWALYYLVGGDWVFGDALCKL	59
40	Query:	116	WVAFDIMCSTASILNLCVISVARYWAIISRPFRYERKMTQRMALVMVRPAWTLSLISFIP + + + + + +	175
	Sbjct:	60	VGALFVVNGYASILLTAISIDRYLATVHPLRYRRIRTPRRRAKVLLLVWVLALLSLPP	119
	Query:	176	VQLNWHRDQAVSWGGLDLPPNNLANWTPWEEAVWEPDVRAENCDSLLNRTYAISSLISFY + + + + + + + + + +	235
45	Sbjct:	120	LLFWSLRL-----TVEEGNTVCLIDFPEE-----SVKRYSVLLSTLVGFV	159
	Query:	236	IPMAIMIVTYTRIYRIAQVQIRRSSLERAEEHVQSCRSSAGCTPDTSLRFSIKKSTEVL + + + + + * + + +	295
	Sbjct:	160	LPLLVLVLCYTRILRTLKRARSQ-----RSLKRSSSERKAA	197
50	Query:	296	KTLSVIMGVFVCCWLPPFILNCMVPPCSGHPKGPPAGFPCVSETTFDVFIFCWANSSLN + + + + + + +	355
	Sbjct:	198	KMLLVVVVFVLCWLPLYHIVLVLDSLC-----LLSIWRVLPFTALLITLWLAYVNNSCLN	250
55	Query:	356	PV 357 +	

Sbjct: 251 PI 252

NOV5 also has homology to proteins found in the patp patent database as shown in Table 5E.

5

Table 5E. BLAST results for NOV5 for patp Database					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
patp:AAR22546	Truncated Dopamine D1 receptor encoded by pseudogene clone GL-39 Homo sapiens	479	453/480 (94%)	460/480 (95%)	1.7e- 244
patp:AAR79381	Dopamine receptor D5 - Homo sapiens	477	436/480 (90%)	445/480 (92%)	2.0e- 236

The rhodopsin-like GPCRs themselves represent a widespread protein family that includes hormone, neurotransmitter and light receptors, all of which transduce extracellular signals through interaction with guanine nucleotide-binding (G) proteins. Although their activating ligands vary widely in structure and character, the amino acid sequences of the receptors are very similar and are believed to adopt a common structural framework comprising 7 transmembrane (TM) helices.

G-protein-coupled receptors (GPCRs) constitute a vast protein family that encompasses a wide range of functions (including various autocrine, paracrine and endocrine processes). They show considerable diversity at the sequence level, on the basis of which they can be separated into distinct groups. The term clan is used to describe the GPCRs, as they embrace a group of families for which there are indications of evolutionary relationship, but between which there is no statistically significant similarity in sequence. The currently known clan members include the rhodopsin-like GPCRs, the secretin-like GPCRs, the cAMP receptors, the fungal mating pheromone receptors, and the metabotropic glutamate receptor family.

The diverse physiologic actions of dopamine are mediated by its interaction with 2 types of G protein-coupled receptor, D1 and D2, which stimulate and inhibit, respectively, the enzyme adenylyl cyclase. Three groups reported the cloning of the D1 dopamine receptor gene (Dearry et al., 1990 ; Zhou et al., 1990 ; Sunahara et al., 1990). The gene encodes a protein of 446 amino acids having a predicted relative molecular mass of 49,300 and a transmembrane topology similar to that of other G protein-coupled receptors. Northern blot analysis and *in situ* hybridization showed that the mRNA for this receptor is most abundant in caudate, nucleus

accumbens and olfactory tubercle, with little or no mRNA detectable in substantia nigra, liver, kidney, or heart (Dearry et al., 1990). Sunahara et al. (1990) reported that the DRD1 gene is intronless and, by Southern blot hybridization to DNAs from a hybrid cell panel, they mapped the gene to chromosome 5. Family linkage studies confirmed this assignment and suggested
5 that it is in the same general region as the gene for glucocorticoid receptor and D5S22, a marker about 12 cM from GRL. This places it in the 5q31-q34 region near the structurally homologous genes for beta-2-adrenergic receptor and alpha-1-adrenergic receptor. Using pulsed field gel electrophoresis and a range of different restriction enzyme digests, Boultwood et al. (1991) established that GRL and DRD1 are on the same 300-kb genomic DNA fragment.
10 Grandy et al. (1990) used the recently cloned DRD1 gene to map the locus to chromosome 5 in rodent-human somatic cell hybrids. Fluorescence in situ hybridization refined the localization to 5q35.1. A 2-allele EcoRI RFLP associated with DRD1 allowed confirmation of the localization by linkage analysis in CEPH families. The homologous gene in the mouse is located on chromosome 13.

15 The distal end of 5q, 5q31.1-qter, contains the genes for 2 adrenergic receptors, ADRB2 and ADRA1B and the dopamine receptor type 1A gene. Krushkal et al. (1998) used an efficient discordant sib-pair ascertainment scheme to investigate the impact of this region of the genome on variation in systolic blood pressure in young Caucasians. They measured 8 highly polymorphic markers spanning this positional candidate gene-rich region in 427
20 individuals from 55 3-generation pedigrees containing 69 discordant sib pairs, and calculated multipoint identity by descent probabilities. The results of genetic linkage and association tests indicated that the region between markers D5S2093 and D5S462 was significantly linked to 1 or more polymorphic genes influencing interindividual variation in systolic blood pressure levels. Since the ADRA1B and DRD1A genes are located close to these markers, the data
25 suggested that genetic variation in 1 or both of these G protein-coupled receptors, which participate in the control of vascular tone, plays an important role in influencing interindividual variation in systolic blood pressure levels

The disclosed NOV5 nucleic acid of the invention encoding a Dopamine receptor -like protein includes the nucleic acid whose sequence is provided in Table 5A or a fragment
30 thereof. The invention also includes a mutant or variant nucleic acid any of whose bases may be changed from the corresponding base shown in Table 5A while still encoding a protein that maintains its Dopamine receptor -like activities and physiological functions, or a fragment of such a nucleic acid. The invention further includes nucleic acids whose sequences are complementary to those just described, including nucleic acid fragments that are

complementary to any of the nucleic acids just described. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications. Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject. In the mutant or variant nucleic acids, and their complements, up to about 10% percent of the bases may be so changed.

The disclosed NOV5 protein of the invention includes the Dopamine receptor -like protein whose sequence is provided in Table 5B. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in Table 5B while still encoding a protein that maintains its Dopamine receptor -like activities and physiological functions, or a functional fragment thereof. In the mutant or variant protein, up to about 34% percent of the residues may be so changed.

The NOV5 nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in schizophrenia, and other dopamine-dysfunctional states, Hypertension, Huntington's disease, levodopa-induced dyskinesias, alcoholism, Diabetes Insipidus and Mellitus with Optic Atrophy and Deafness, Wolfram Syndrome and/or other pathologies and disorders. For example, a cDNA encoding the dopamine receptor-like protein may be useful in gene therapy, and the dopamine receptor-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from schizophrenia, and other dopamine-dysfunctional states, Hypertension, Huntington's disease, levodopa-induced dyskinesias, alcoholism, Diabetes Insipidus and Mellitus with Optic Atrophy and Deafness, Wolfram Syndrome, as well as other diseases, disorders and conditions. The NOV5 nucleic acid, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

NOV5 nucleic acids and polypeptides are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-NOVX Antibodies" section below. For example the disclosed NOV5 protein have multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, contemplated NOV5

epitope is from about amino acids 1 to 10. In other embodiments, NOV5 epitope is from about amino acids 125 to 150, from about amino acids 175 to 230, from about amino acids 250 to 300, from about amino acids 320 to 330, from about amino acids 350 to 370, from about amino acids 380 to 410, or from about amino acids 420 to 460. This novel protein also has 5 value in development of powerful assay system for functional analysis of various human disorders, which will help in understanding of pathology of the disease and development of new drug targets for various disorders.

NOV6

10 A disclosed NOV6 nucleic acid of 2657 nucleotides (also referred to as GM523_e_1_A) encoding a novel Metabotropic Glutamate Receptor-like protein is shown in Table 6A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 6-8 and ending with a TGA codon at nucleotides 2643-2645. A putative untranslated region upstream from the initiation codon and downstream from the termination 15 codon is underlined in Table 6A, and the start and stop codons are in bold letters.

Table 6A. NOV6 Nucleotide Sequence (SEQ ID NO:16)

<pre> GATTCAAGAGATGTGACAAGACTACAAGTTTATGTTAGCTTGTGTTCAAGGGATTTAGTC TTTAGGAGATCACAACTTATGAGGGAGAAATTAAAATAGAAGGAGACCTTGTGTTAGGGGCTATT CCTATTAAATGAAAAGGCACTGGAACGTGAAGAGTGAGCAGAATCAATGAAGACAGAGGTATCAAACGCC TGGAGGCCATGTTGTTGCCATTGATGAAATCAACAAAGACAATTACTTGCTTCAGGAGTGAAGCTGGG GGTTCACATTGGATACTGTTCAAGAGACACCTATGCATTAGACAGTCAGTGGAGTTTGCTAGAGCA TCGTTGACTAAAGGGATGGAAGCTATATGTCCTGATGGCATATGCTATTCAAGAAAACATCC CACTACTCATTGCAAGGAGTCATTGGCGGTTGTAACAGCAGTGTTCATACAGTAGCAAACTTGCTGAG GCTCTTCAGATCCTCAGATAAGCTACGCCCTCACCAGTGCACAACTCAGGCCAAATCGCCATATGAT TATTTGGCAGGACCGTGGCCCTGACTTCTACCAAGGCCAACGCCATGGCGAGATTTGCGCTACTTTA ACTGGACCTATGTTGTCACGTGCTCTGAAGGTGACTATGGGAGACAGGGATTGAGGCCCTCGAGCA GGAAGCAGGCTACGCCAACATCTGCATCGCACTGCTGAAAAGGTGGGCCCTCAACATCCGCAAGTCC TACGACACCGTGATCCGGTGAAGCTCTGGAGCAAGAACCTAACCGCGCGTGTGGCTCTGTTCATGCCAGTG ATGACTCACCGAGACTTGATGCCCTGCAAGCCAGCGGTGAATGCTTCCCTCACCTGGGTGGCAAGTGG CTGGGGTGCACAGGAGAGCATTTGTCAGGGCAGTGACGACGTCGCCATGGAGCCATCACCTGGAGCTG GCGTCCCACCTGTTGTCAGTTGATCGCTACTTCCAGAGCCTCAACCCCTAACAAATCATCGTAACC CCTGGGTCGGAGCTTCTGGGAGCAGAAGCTTCCAGTGCAGCCTCCAGAACAGAGAAACACAGACAGAT TTGTGACAAGCACCTGGCATTGACAGCAGCAACTATGAAAGAATCCAAGATCATGTTGTTGCTGAAT GCAGTGTATGCCATGGCGCATGCCCTGCAAAATGCAACGCCACCCCTGTGCTCCAAACACCAAGCTCT GTGATGCAATGAAGATCCTGGATGAGAAAGAGTTGATCAAAGATTATTGCTGAAATCAACTCCCTGC TCCATTCAACCCAAATAAAGGAGCAGACGATTGTGAAGTTGACACTTACGGAGACGGGATGGGAAGA TACAACCGTCAACTTCCAGCATATAGTGGAAAGTATTCCCTACTTAAAGTTGGCCACTGGGAGAAA CTTATATCTAGATGTGACTCTATTCTATGGTCCCGGAACCTAGCTCCCACCTCCAGTGCAGTGATCC CTGTGCCCAATGAAATGAAAACATGCAAGCCAGGAGATGTTGCTGCTGGATCTGCATCCCAATGTGAG CCCTATGAATACTGGTGTGAGTTCACCTGCATGGATTGTCGCCCTGGCCAGTGGCCCACTGCAGACCC TATCTGGATGCTACACCTCCAGAGGATTACATCAGGTGGGAAGATGCCCTGGCAATAGGCCAGTCAC TATTGCTGCTGGTTTATGTGTAATGCATAGTCATACTGTTTATCAAGCAACAAACACACCC TTGGTCAAAGCATCAGGGCGAGAACTCTGCTACATCTGTTATTTGGAGTTAGCCTGTCCTATIGCATGA CATTCCTCTCATGCTAACGCCATGCCGTGTCATCTGTCATGCCCTGCACTGGGCTTGGGACCTCCTT TGCCATCTGTTATTCAGCTCTCTGCACCAAGACAAACTGCATCGCTCGCATCTTGATGGGGTCAAGAAT GGCGCTCAGAGGCCAAATTCACTCAGCCCCAGTTCTCAGGTTTATCTGCTGGTTGATACTGGTGC AAATTGTGATGGTGTCTGTTGCTTATCTGGAGACTCCAGTACTAGAAGATAACCCCTGCCAGAGAA GCGGGAAAACAGTCATCTAAATGCAATGTCAAACAGATCCAGCATGTTGATCTCTGACCTATGACGTG GTTCTGGTGTATTCTATGCACTGTGTTATGCTTCAAACAGGAAGTGTCTGAAACTTCAATGAAGCCA AGTTCATAGGCTTACCCATGTCACCAACCTGCATCATCTGGTTGGCATTCCTCCATATTGAC </pre>
--

ATCAAGTGACTACAGAGTACAGAGCACAACAACTGTGATCTCCGTAGCTTGAGTGGTTCTGGTCTTG
GCCGTTGTTGCCCCCAAGGCTCACATTGCTCTTCACACCCGAAAGAATGCTGCACACACAGAC
TTAACCTCAACAGGTCTAGTGTCTGGAACTGCGAACACATATTCTCAGGCTCTGCAAGCACGTATGT
GCCAACGGTGTGCAATGGGGGGAGTCTCGACTCACCACCTCATCTCTGTATGTTGAATTGCA

The disclosed NOV6 nucleic acid sequence has 2522 of 2658 bases (94%) identical to a Rat metabotropic glutamate receptor 3 mRNA from *Rattus norvegicus* (GENBANK-ID: M92076) ($E = 0.0$).

- 5 A disclosed NOV6 polypeptide (SEQ ID NO:17) encoded by SEQ ID NO:16 is 879
amino acid residues and is presented using the one-letter amino acid code in Table 6B. Signal
P, Psort and/or Hydropathy results predict that NOV6 contains a signal peptide and is likely to
be localized in the endoplasmic reticulum (membrane) with a certainty of 0.6850. In other
embodiments, NOV6 is also likely to be localized to the plasma membrane with a certainty of
10 0.6400, to the Golgi body with a certainty of 0.4600, or to the endoplasmic reticulum (lumen)
with a certainty of 0.1000. The most likely cleavage site for a NOV6 peptide is between amino
acids 24 and 25, at: SLG-DH.

Table 6B. Encoded NOV6 protein sequence (SEQ ID NO:17).

MKMLTRLQVLMALAFSKGLVSLGHDHFMRRREIKIEGDLVLGGLPFNEKGTCRINEDERGICRLEAMLF
IDEINKDNYLLPGVKLGHVILDTCSRDTYALEQSLEFVRASLTKVDEAEMCPDGSYAIQENIPLLIAGVIGGSY
SSVSIQVANLRLFQIPQISYASTSAKLSDKSRVDYFARTVPDPFYQAKAMAELIRYFNWTVYSTVASESGDYGET
GIEAFEQEARLNRCIATAEKVGSRNSIRKSYSVDRFLNRLQPKNARVVFLFMRSDSRELIAASRVNAWSFTWAS
DGWGAQESIVKGSEHVAQGAIITLEASHPVRFQDRYFQOSLNPYNNHRNPWFPRDFWQKFQCSLQKNRHNQICDK
HLAIDDSNVEQESKIMFVNNAVAYAMAHALHKMORTLCPCNTTCKLCDAMKILDGKKLYKDYLKINFLAPFPNPKGA
DSIVKFDTYGDGMGRYNVNFQHIGGKYSYLVKGHWAEITLYLDVDSIHWSRNSVPTSQCSDPCAPNEMKNMQPGD
VCCWICIPCEPEYELVDBEFTCMDCGPQGWPTADLSCGYNLPEDYIRWEADAIAIGPVTIACLGFMCCTIVITVF
HNNTPLVKASGRRELCYLLFGVSLSYCMTFFFIAKPSPVICALRRIGLGTSAICYSALLTKTNCIARIFDGVKN
GAQRPKFISPPSQVFICLGLILVQIVMVSVWLLIETPTGTRYTLPEKRETRVILCKCNVKDSSMIISLTYDVVLVIL
CTVYAFKTRKCPENFNEAKFIGFTMYCTTIIWLAFPLPFTVTSYDVRQTTMCISVSLSGFVVLGCLFAPKVI
VLEPOOKNUVYTHRLJHNFESVSGTATTYSOASASTVYPTVCNGREVLJSTTSSJ

- 15 The disclosed NOV6 amino acid sequence has 877 of 879 amino acid residues (99%) identical to, and 878 of 879 amino acid residues (99%) similar to, the 879 amino acid residue METABOTROPIC GLUTAMATE RECEPTOR 3 PROTEIN protein from *Mus musculus* (Mouse (Q9QYS2) (E = 0.0).

NOV6 also has homology to the amino acid sequences shown in the BLASTP data listed in Table 6C.

Table 6C. BLAST results for NOV6

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
---------------------------	-------------------	----------------	-----------------	------------------	--------

gi 400254 sp P31422 MGR3_RAT	METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR	879	864/879 (98%)	874/879 (99%)	0.0
gi 6288800 gb AAF06 741.1 AF170701_1	metabotropic glutamate receptor 3 protein [Mus musculus]	879	877/879 (99%)	878/879 (99%)	0.0
gi 11279202 pir JC 7160	metabotropic glutamate receptor subtype 3 precursor - mouse	879	875/879 (99%)	876/879 (99%)	0.0

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 6D.

Table 6D Information for the ClustalW proteins

- 5 1) NOV6 (SEQ ID NO:17)
2) gi|400254|sp|P31422|MGR3_RAT METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR (SEQ ID
NO:52)
3) gi|6288800|gb|AAF06741.1|AF170701_1 metabotropic glutamate receptor 3 protein
[Mus musculus] (SEQ ID NO:53)
10 4) gi|11279202|pir||JC7160 metabotropic glutamate receptor subtype 3 precursor -
mouse (SEQ ID NO:54)

		10	20	30	40	50		
15	NOV6 gi 400254 gi 6288800 gi 11279202	MKMLTRIQLVLMALFSKGFLVSLGDHNFMREI KIEGDLVLGCLFPINEK MKMLTRIQLVLMALFSKGFLVSLGDHNFMREI KIEGDLVLGCLFPINEK MKMLTRIQLVLMALFSKGFLVSLGDHNFMREI KIEGDLVLGCLFPINEK MKMLTRIQLVLMALFSKGFLVSLGDHNFMREI KIEGDLVLGCLFPINEK					
20		60	70	80	90	100
	NOV6 gi 400254 gi 6288800 gi 11279202	GTGTTECGRINE D RGIQRLEAMLFAIDEINKDNYLPGVVKLGVHILDTC S GTGTTECGRINE D RGIQRLEAMLFAIDEINKDNYLPGVVKLGVHILDTC S GTGTTECGRINE D RGIQRLEAMLFAIDEINKDNYLPGVVKLGVHILDTC S GTGTTECGRINE D RGIQRLEAMLFAIDEINKDNYLPGVVKLGVHILDTC S						
25		110	120	130	140	150
	NOV6 gi 400254 gi 6288800 gi 11279202	RDTYALEQSLEFVRASLT K VDEA EY CPDGSYA I QENIP L LIAGVIGGSY RDTYALEQSLEFVRASLT K VDEA EY CPDGSYA I QENIP L LIAGVIGGSY RDTYALEQSLEFVRASLT K VDEA EY CPDGSYA I QENIP L LIAGVIGGSY RDTYALEQSLEFVRASLT K VDEA EY CPDGSYA I QENIP L LIAGVIGGSY						
30		160	170	180	190	200
	NOV6 gi 400254 gi 6288800 gi 11279202	SSVSIVQVANLLRLFQIPOQISYASTSAKLS D KSRYDYFARTVPPDFYQAKA SSVSIVQVANLLRLFQIPOQISYASTSAKLS D KSRYDYFARTVPPDFYQAKA SSVSIVQVANLLRLFQIPOQISYASTSAKLS D KSRYDYFARTVPPDFYQAKA SSVSIVQVANLLRLFQIPOQISYASTSAKLS D KSRYDYFARTVPPDFYQAKA						
35		210	220	230	240	250
	NOV6 gi 400254 gi 6288800 gi 11279202	MAEILRYFNWTYVSTVASE G DYGET G IEAFEQEARLRN C IATA E KVGRS MAEILRLFNWTYVSTVASE G DYGET G IEAFEQEARLRN C IATA E KVGRS MAEILRYFNWTYVSTVASE G DYGET G IEAFEQEARLRN C IATA E KVGRS MAEILRYFNWTYVSTVASE G DYGET G IEAFEQEARLRN C IATA E KVGRS						
40		260	270	280	290	300
	NOV6 gi 400254 gi 6288800 gi 11279202	NIRKSYSDVIRELLQKPNARVVVLFMRSDDSRELIAASRVNASFTWVAS						
45								
50								

gi 400254	NIRKSYDSVIRELLQKPNAARVVVLFMRSDDSRELIAAANRVNASFTWVAS
gi 6288800	NIRKSYDSVIRELLQKPNAARVVVLFMRSDDSRELIAAASRVNASFTWVAS
gi 11279202	NIRKSYDSVIRELLQKPNAARVVVLFMRSDDSRELIAAASRVNASFTWVAS
5	310 320 330 340 350
NOV6	DGWGAQESIVKGSEHVAYGAITLEELASHPVRFQDFRQFQSINPYNNHHRNPW
gi 400254	DGWGAQESIVKGSEHVAYGAITLEELASHPVRFQDFRQFQSINPYNNHHRNPW
gi 6288800	DGWGAQESIVKGSEHVAYGAITLEELASHPVRFQDFRQFQSINPYNNHHRNPW
10	gi 11279202 DGWGAQESIVKGSEHVAYGAITLEELASHPVRFQDFRQFQSINPYNNHHRNPW
	360 370 380 390 400
15	NOV6 FRDFWEQKFCQSLQNKRNRHQICDKHLAIDSSNYEQESKIMFVVNAVYAM
gi 400254	FRDFWEQKFCQSLQNKRNRHQICDKHLAIDSSNYEQESKIMFVVNAVYAM
gi 6288800	FRDFWEQKFCQSLQNKRNRHQICDKHLAIDSSNYEQESKIMFVVNAVYAM
gi 11279202	FRDFWEQKFCQSLQNKRNRHQICDKHLAIDSSNYEQESKIMFVVNAVYAM
20	410 420 430 440 450
NOV6	AHALHKMQRITLCPTNTKLCDAMKILDGKKLYKDYLKINFAPFPNPKGA
gi 400254	AHALHKMQRITLCPTNTKLCDAMKILDGKKLYKDYLKINFAPFPNPKGA
gi 6288800	AEALHKMQRITLCPTNTKLCDAMKILDGKKLYKDYLKINFAPFPNPKGA
gi 11279202	AHALHKMQRITLCPTNTKLCDAMKILDGKKLYKDYLKINFAPFPNPKGA
25	460 470 480 490 500
NOV6	DSIVKFDTYGDCGMGRYNVNFQHIGGKSYLKVGHWETLYLDVDSTIHWS
gi 400254	DSIVKFDTEGDCGMGRYNVNFQHIGGKSYLKVGHWETLSLDVDSTIHWS
gi 6288800	DSIVKFDTYGDCGMGRYNVNFQHIGGKSYLKVGHWETLSLDVDSTIHWS
gi 11279202	DSIVKFDTYGDCGMGRYNVNFQHIGGKSYLKVGHWETLYLDVDSTIHWS
35	510 520 530 540 550
NOV6	RNSVPSTSQCSDPCAPNEMKNMQPGDVCWCICIPCEPYEYLDEFTCMDCG
gi 400254	RNSVPSTSQCSDPCAPNEMKNMQPGDVCWCICIPCEPYEYLDEFTCMDCG
gi 6288800	RNSVPSTSQCSDPCAPNEMKNMQPGDVCWCICIPCEPYEYLDEFTCMDCG
gi 11279202	RNSVPSTSQCSDPCAPNEMKNMQPGDVCWCICIPCEPYEYLDEFTCMDCG
40	560 570 580 590 600
NOV6	PGQWPTADLSCGCYNLPEDYIWRWEDAWAIGPVTIACLGFMCTCIVITVFIK
gi 400254	PGQWPTADLSCGCYNLPEDYIWRWEDAWAIGPVTIACLGFMCTCIVITVFIK
gi 6288800	PGQWPTADLSCGCYNLPEDYIWRWEDAWAIGPVTIACLGFMCTCIVITVFIK
45	gi 11279202 PGQWPTADLSCGCYNLPEDYIWRWEDAWAIGPVTIACLGFMCTCIVITVFIK
	610 620 630 640 650
50	NOV6 HNNTPPLVKASGRELCYILLFGVSLSYCMTFFFIAKPSPVICALRRRLGLGT
gi 400254	HNNTPPLVKASGRELCYILLFGVSLSYCMTFFFIAKPSPVICALRRRLGLGT
gi 6288800	HNNTPPLVKASGRELCYILLFGVSLSYCMTFFFIAKPSPVICALRRRLGLGT
gi 11279202	HNNTPPLVKASGRELCYILLFGVSLSYCMTFFFIAKPSPVICALRRRLGLGT
55	660 670 680 690 700
NOV6	SFAICYSALLTKTNCIARIFDGVKNGAQRPKFISPSSQVFICLGLLILVQI
gi 400254	SFAICYSALLTKTNCIARIFDGVKNGAQRPKFISPSSQVFICLGLLILVQI
gi 6288800	SFAICYSALLTKTNCIARI
gi 11279202	FDGVKNGAQRPKFISPSSQVFICLGLLILVQI
60	710 720 730 740 750
NOV6	VMVSVWLILETFGTRRYTLPEKRETVILKCNVKDSSMLISLTYDVVLVIL
gi 400254	VMVSVWLILETFGTRRYTLPEKRETVILKCNVKDSSMLISLTYDVVLVIL
gi 6288800	VMVSVWLILETFGTRRYTLPEKRETVILKCNVKDSSMLISLTYDVVLVIL
gi 11279202	VMVSVWLILETFGTRRYTLPEKRETVILKCNVKDSSMLISLTYDVVLVIL
70	760 770 780 790 800
NOV6	CTVYAFKTRKCPENFNEAKFIGFTMYTTCIIWLAFLPIFYVTSSDYRVQI

20

Table 6E-F lists the domain description from DOMAIN analysis results against NOV6. This indicates that the NOV6 sequence has properties similar to those of other proteins known to contain this domain.

Table 6E. Domain Analysis of NOV6

gnl|Pfam|pfam01094, ANF receptor, Receptor family ligand binding region. This family includes extracellular ligand binding domains of a wide range of receptors. This family also includes the bacterial amino acid binding proteins of known structure. (SEQ ID NO:84)
CD-Length = 402 residues, 98.5% aligned
Score = 323 bits (827), Expect = 3e-89

Sbjct: 383 ETGQLKVTGTYDGVGKWTE 401

Table 6F. Domain Analysis of NOV6

gnl|Pfam|pfam00003, 7tm_3, 7 transmembrane receptor (metabotropic E family). (SEQ ID NO:85)
CD-Length = 256 residues, 100.0% aligned
Score = 323 bits (827), Expect = 3e-89

5	Query:	576	WAIGPVTIACLGFMCTCIVITVFIKHNNTPLVKASGRELVCYILLFGVSVLSYCMFFFIAK + + + + + + + +	635
	Sbjct:	1	LGIVLVALAVLGIVLTLFVLVVFVKHRDTPIVKASNRELSYLLIGLILCYCSFLFIGK	60
10	Query:	636	PSPVICALRRLGLGTSFAICYSALLTKTNCIARIFDGVKNGAQRPKFIFSPSSQVFICLGL + + + + +	695
	Sbjct:	61	PSETSCILRRILFGLGFITLCYSSLAKTNRVLRIFRRAKPGSGPKFKFIFSPWAQVLIVLIL	120
	Query:	696	ILVQIVMVSVWLILETPGTRRYTLPEKRETIVLKCNVKDS-SMLISLTVDVVLVILCTVV + + + + + + + + + + + + +	754
15	Sbjct:	121	VLIQVIICVIWVVEPPRPTIDYSEKEK-IILECNKGSMVAFFVVVLGYDGLLAVLCTPL	179
	Query:	755	AFKTRKCBENFNEAKFIGFTMYTTCIIWIWLAFLPIFYVTSSDYRQTTTM CISVSLSGFVV + + + + + + +	814
	Sbjct:	180	AFLTRNLPENFNEAKFIGFSMLTFCIVWWAFIPIYL--STPGKVQVAVEIFSILASSTVL	237
20	Query:	815	LGCLFAPKVHIVLFQPQKN 833 + + + +	
	Sbjct:	238	LGCLFVPKCYIILFRPEKN 256	

25 G-protein-coupled receptors (GPCRs) constitute a vast protein family that encompasses a wide range of functions (including various autocrine, paracrine and endocrine processes). They show considerable diversity at the sequence level, on the basis of which they can be separated into distinct groups. The term clan is used to describe the GPCRs, as they embrace a group of families for which there are indications of evolutionary relationship, but between which there is no statistically significant similarity in sequence. The currently known clan members include the rhodopsin-like GPCRs, the secretin-like GPCRs, the cAMP receptors, the fungal mating pheromone receptors, and the metabotropic glutamate receptor family.

The metabotropic glutamate receptors are functionally and pharmacologically distinct from the ionotropic glutamate receptors. They are coupled to G-proteins and stimulate the inositol phosphate/Ca²⁺ intracellular signalling pathway. The amino acid sequences of the receptors contain high proportions of hydrophobic residues grouped into 7 domains, in a manner reminiscent of the rhodopsins and other receptors believed to interact with G-proteins. However, while a similar 3D framework has been proposed to account for this, there is no significant sequence identity between these and receptors of the rhodopsin-type family: the

metabotropic glutamate receptors thus bear their own distinctive '7TM' signature. This 7TM signature is also shared by the calcium-sensing receptors, and GABA (gamma-amino-butyric acid) type B (GABA(B)) receptors.

At least eight sub-types of metabotropic receptor (MGR1-8) have been identified in cloning studies. The sub-types differ in their agonist pharmacology and signal transduction pathways.

The mGluR3 gene consists of six exons and spans over 95 kb. Exon 1 and its preceding putative promoter are located distantly from the following protein-coding region. In the mGluR family, mGluR3 and mGluR5 are both expressed in neuronal and glial cells and are upregulated during the early postnatal period. They are, however, coupled to two distinct signaling cascades and have been shown to exert opposite influences on some functions of cultured astrocytes. In cultured astrocytes, mGluR3 and mGluR5 mRNA levels were significantly increased by exposure to epidermal growth factor (EGF), basic fibroblast growth factor (bFGF), or transforming growth factor-alpha; and EGF was more efficacious than bFGF in producing this increase. Hence, mGluR3 and mGluR5 mRNAs are concertedly upregulated in cultured astrocytes by specific growth factors. This finding suggests that the two mGluR subtypes may play an important role in maintaining the proper balance of astrocyte functions via two distinct signal transduction mechanisms.

Glutamate receptors are divided into 2 distinct classes: ionotropic glutamate receptors (iGluRs) and metabotropic glutamate receptors (mGluRs). The iGluRs consist of N-methyl-D-aspartate (NMDA) receptors and non-NMDA receptors. Non-NMDA receptors are further subdivided into 2 groups: alpha-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid receptors and kainate receptors. The mGluRs are divided into 3 groups according to agonist selectivity, coupling to different effector systems, and sequence homology. Group I includes mGluR1 and mGluR5, which are coupled to inositol phospholipid metabolism. Group II, which includes mGluR2 and mGluR3, and group III, which includes mGluR4, mGluR6, mGluR7, and mGluR8, are negatively coupled to adenylate cyclase activity. Each mGluR possesses a large extracellular domain. Okamoto et al. (1998) expressed mGluR1-alpha (mGluR1A) in insect cells on a baculovirus system. They isolated a soluble mGluR that encodes only the extracellular domain and retains a ligand binding characteristic similar to that of the full-length receptor. Their observations demonstrated that a ligand binding event in mGluRs can be dissociated from the membrane domain.

Smitt et al. (2000) demonstrated that autoantibody against mGluR1A was responsible for severe paraneoplastic cerebellar ataxia in 2 patients. The disorder developed in both patients while they were in remission from Hodgkin disease. One, a teenager, had been in remission for 2 years when truncal ataxia, intention tremor, and gait ataxia developed. This 5 patient improved clinically with loss of cells in the cerebrospinal fluid when treated with plasma exchanges, oral prednisone, and 2 courses of intravenous immune globulin. The second patient reported by Smitt et al. (2000) was in her late forties and, in addition to successfully treated Hodgkin disease, had polycystic kidney disease requiring hemodialysis for many years. Therapy was less successful in this patient, possibly because of delay in initiation.

10 The disclosed NOV6 nucleic acid of the invention encoding a Metabotropic Glutamate Receptor -like protein includes the nucleic acid whose sequence is provided in Table 6A or a fragment thereof. The invention also includes a mutant or variant nucleic acid any of whose bases may be changed from the corresponding base shown in Table 6A while still encoding a protein that maintains its Metabotropic Glutamate Receptor -like activities and physiological 15 functions, or a fragment of such a nucleic acid. The invention further includes nucleic acids whose sequences are complementary to those just described, including nucleic acid fragments that are complementary to any of the nucleic acids just described. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications. Such modifications include, by way of nonlimiting example, 20 modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject. In the mutant or variant nucleic acids, and their complements, up to about 10% percent of the bases may be so changed.

25 The disclosed NOV6 protein of the invention includes the Metabotropic Glutamate Receptor -like protein whose sequence is provided in Table 6B. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in Table 6B while still encoding a protein that maintains its Metabotropic Glutamate Receptor -like activities and physiological functions, or a functional fragment 30 thereof. In the mutant or variant protein, up to about 10% percent of the residues may be so changed.

The above defined information for this invention suggests that these Metabotropic Glutamate Receptor -like proteins (NOV6) may function as a member of a "Metabotropic Glutamate Receptor family". Therefore, the NOV6 nucleic acids and proteins identified here

may be useful in potential therapeutic applications implicated in (but not limited to) various pathologies and disorders as indicated below. The potential therapeutic applications for this invention include, but are not limited to: protein therapeutic, small molecule drug target, antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), diagnostic and/or prognostic marker, gene therapy (gene delivery/gene ablation), research tools, tissue regeneration *in vivo* and *in vitro* of all tissues and cell types composing (but not limited to) those defined here.

The nucleic acids and proteins of NOV6 are useful in potential therapeutic applications implicated in immune disorders and airway pathologies such as epileptic seizures and other neurological disorders, Hodgkin disease, polycystic kidney disease, mental depression, Adenocarcinoma, Smith-Lemli-Opitz syndrome, Retinitis pigmentosa, and/or other pathologies and disorders. For example, a cDNA encoding NOV6 may be useful in gene therapy, and NOV6 may be useful when administered to a subject in need thereof. By way of nonlimiting example, NOV6 will have efficacy for treatment of patients suffering from epileptic seizures and other neurological disorders, Hodgkin disease, polycystic kidney disease, mental depression, Adenocarcinoma, Smith-Lemli-Opitz syndrome, Retinitis pigmentosa. The novel NOV6 nucleic acid encoding NOV6 protein, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

NOV6 nucleic acids and polypeptides are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-NOVX Antibodies" section below. For example the disclosed NOV6 protein have multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, contemplated NOV6 epitope is from about amino acids 20 to 30. In other embodiments, NOV6 epitope is from about amino acids 50 to 70, from about amino acids 100 to 140, from about amino acids 180 to 200, from about amino acids 210 to 280, from about amino acids 310 to 400, from about amino acids 450 to 510, from about amino acids 520 to 560, from about amino acids 600 to 610, from about amino acids 660 to 680, from about amino acids 700 to 720, from about amino acids 750 to 770, or from about amino acids 800 to 850. This novel protein also has value in development of powerful assay system for functional analysis of various human

disorders, which will help in understanding of pathology of the disease and development of new drug targets for various disorders.

NOV7

5 NOV7 includes three novel PV-1-like proteins disclosed below. The disclosed proteins have been named NOV7a, NOV7b, and NOV7c.

NOV7a

A disclosed NOV7a nucleic acid of 1366 nucleotides (also referred to sggc_draft_ba560a15_20000723_da1) encoding a novel PV-1-like receptor protein is shown 10 in Table 7A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TGA codon at nucleotides 1327-1329. In Table 7A, the 3' untranslated region is underlined and the start and stop codons are in bold letters.

Table 7A. NOV7a Nucleotide Sequence (SEQ ID NO:18)

```

ATGGGTCTGCCATGGACACGGACGGTCTACGCTCGGGGGGGAGCTCTCGGGCTCTGGTATTA
CCTCGCTACTTCCCTCTCGTCTCCCATCCATTCATCCTCGTCTCTTATGG
TCTATGGCAACGTGAGCACAGAGTCCAACCTCAGGCCAACCTGACCAAGGAGCTCAACITCACCACCCGCCAA
AGTCAGCTCTAGGGCTCACGGCTCCAGTCCAATTGACCAAGGAGCTCAACITCACCACCCGCCAA
GGATGCCATCATGCAGATGTGGCTGAATGCTGCCGACCTGGACCGCATCAATGCCAGCTCCGCCAGT
GCCAGGGTACCGGTAATCTACAGAACATCAGAGTACATGGCTGCCATCATCTTGAGTGAGAAGCAA
TGCAGAGATCAATTCAAGGACATGAACAAAGAGCTGCGATGCCCTTGCTCTTATGCTGAATCAGAAGGTTGAA
GACGCTGGGGTGGAGATAGCCAAGGAGAACCCATTGCACTAAAGGATAAGGAAAGCCTGCTGAACA
AACCGTGGCGGAGGAACAGCTGGTTGAATGGTGAACACCCGGGAGCTGAGCACCAAGACGCCACGTG
GCCAAGGAGCAACTGCAAAGGGTCAAGCCCTCTGCCCTGGACAAGGACAAGTTGAGATGGACCT
TCGTAACCTGTGGAGGGACTCCATTATCCCACCGCAGCTGGAACACCTGGTTAACACCTCTACCATCCCC
TGGGCTCGGAAATTGGCTCCATCCGAGGCTGCGACACATGCCAGCTCAAGGCTCAAGGTTGAA
GGTCAGTGGCGGAGCCTCGGGGGATATCGAACCGCTGGCCCGAGAACCTCAGACCTCCAACGCCAGAA
GCTGGAAAGCCCAAGGGGCTGCCAGTCAAGGAGGAGAACAGAAGGTGGAGAAGGAGGCTCAGGCC
GGGAGGCGCAAGCTCAAGCTGAATGCTCCGGCAGACCCAGCTAGCGCTGGAGGAGAACGGGGTGCCTGCC
AAGGAACGAGACAACCTGCCAAGGAGCTGGAAGAGAAGAGAGGGAGGCGGAGCAGCTCAGGATGGAGCT
GGCCATCAGAAAACCTCAGCCCTGGACACCTGCTCATCAAGACCAAGTCAGCCGATGATGCCAGTGTCAAGGC
CCATGGGCTCTGTCCCCAACCCCAAGCCCATCGACCCAGCTAGCCCTGGAGGAGTTCAAGAGGAAGATCCTG
GAGTCCCCAGAGGCCCCCTGCAAGGCATCCCTGAGCCCCATCCAGTGGCTGAGGAGGCTCCGGCACTGACCT
AAGGGCGAATCCCAAGCA

```

15 The disclosed NOV7a nucleic acid sequence, localized to chromosome 19, has 945 of 1345 bases (70%) identical to a 1968 bp PV-1 mRNA from Rattus norvegicus (GENBANK-ID: AF154831|acc:AF154831) ($E = 1.1e^{-121}$).

A disclosed NOV7a polypeptide (SEQ ID NO:19) encoded by SEQ ID NO:18 is 442 amino acid residues and is presented using the one-letter amino acid code in Table 7B. Signal 20 P, Psort and/or Hydropathy results predict that NOV7a has a signal peptide and is likely to be localized in the plasma membrane with a certainty of 0.7900. In other embodiments, NOV7a is also likely to be localized to the nucleus with a certainty of 0.6000, to the microbody (peroxisome) with a certainty of 0.3000, or the Golgi body with a certainty of 0.3000. The

most likely cleavage site for a NOV7a peptide is between amino acids 50 and 51, at: YVG-NV.

SNP data for NOV7a can be found below in Example 3.

Table 7B. Encoded NOV7a protein sequence (SEQ ID NO:19).

```
MGLAMEHGGSYARAGGSRRGCWYYLRYFFLFVSLIQFLIILGLVLFMVYGNVHVSTESNLQATE
RRAEGLYSQQLGLTASQSNLTKELNFTTRAKDAIMQMWLNRDLDLRINASFRQCQGDRVIVTN
NQRYMAII1LSEKQCRDQFKDMNKSCDALLFMLNQKVKTLEVEIAKEKTICTKDKESVLLNKRV
AEEQLVECVKTRELQHQERQLAKEQLQKVQALCFLDKDKFEMDLRNWLWRSIIIPRSLDNLGYN
LYHPLGSELIASIRRACDHMPSLMSSKVEGQCRSLRADIERVARENSDLQRQKLEAQQGLRASQE
AKQKVEKEAQAREAKLQAECSRQTQLALEEKAVLRKERDNLAKELEKKREAEQLRMELAIRNS
ALDTCIKTKSQPMMPVSRPMGPVPNPQPIDPASLEEFKRKILESQRPPAGIPVAPSSG
```

5

The disclosed NOV7a amino acid sequence has 266 of 442 amino acid residues (60%) identical to, and 347 of 442 amino acid residues (78%) similar to, the 438 amino acid residue PV-1 protein from *Rattus norvegicus* (SPTREMBL-ACC:Q9WV78) ($1.6e^{-142}$), and 439 of 442 amino acid residues (99%) identical to, and 439 of 442 amino acid residues (99%) similar to, the 479 amino acid residue Human ORFX ORF1918 polypeptide sequence (patp:AAB42154) ($3.2e^{-229}$).

10

TaqMan data for NOV7a can be found below in Example 2.

NOV7b

A disclosed NOV7b nucleic acid of 1421 nucleotides (also referred to 2847264.0.32) encoding a novel PV-1-like receptor protein is shown in Table 7C. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 55-57 and ending with a TGA codon at nucleotides 1381-1383. In Table 7C, the 5' and 3' untranslated regions are underlines and the start and stop codons are in bold letters.

15

Table 7C. NOV7b Nucleotide Sequence (SEQ ID NO:20)

```
GAATTCTAGGTGGTGGTGAGCAGGGACGGTGACCGGACGGCGGGATCGAGCAAATGGGTCTGCCATGG
GTACGGAGGGTCTACGCTCGGGCGGGGGCAGCTCTCGGGGCTGCTGGTATTACCTCGCGCTACTTCTTCC
TCTTCGTCCTCCATCAATCTCTCATCATCTGGGGCTCGTCTTCTCATGGCTATGGCGACGTGCAC
GTGAGCACAGCTAACCTGCAAGCCACCGCAGCGCCAGGGCTTACAGTCAGCTCTTAGGGCT
CAAGGCCTCCCAGTCCAACCTTGACCAAGGAGCTCAACTTCAACCCACCGCGCAAGGGATGCCATCATGCCAGA
TGTGGCTGAATGCTGCCCGGACCTGGACCGCATCAATGCCAGCTCCGCCAGTGCCAGGGTACCGGGTC
ATCTACACCAACAATCAGAGGTACATGGCTGCCATCATCTTGAGTGAGAAGCAATGCCAGAGATCAATTCAA
GGACATGACAAGAGCTGCCATGCTCTTCATGCTGAATCAGAAGGTGAACAGCAGCTGGAGGTGGAGA
TAGCCAAGGAGAACGACCATGGCAACTAAGGATAAGGAAAGCGTGTGCTGCTGAACAAACAGCGTGGCGGAGGAA
CAGCTGGTTGAATGCCGAAAACCCGGAGCTGCAGCAGCAACAGGCGCAGCTGCCAAGGGAGCACTGCA
AAAGGTGCAAGCCCTCTGCCCTGCCCTGGACAAGGACAAGTTGAGATGGACCTTCTGTAACCTGAGGG
ACTCCATTATCCCACGCGACGCCCTGGACAACCTGGTTACAACCTTACCATCCCCCTGGCTCGGAATTGGCC
TCCATCCGAGAGCTGCGACCAATGCCAGCCTCATGAGCTCCAGGTGGAGGAGCTGGCCCGAGCCT
CCGGGCGGATATCGAACCGCTGGCCCCGGAGAAACTCAGACCTCCAACGCCAGAAGCTGGAAGGCCAGCAGG
GCCTGCGGGGCAGTCAGGAGGCAGAAACAGAAGGTGGAGAAGGGCTCAGGCCGGAGGCCAGCTCCAA
GCTGAATGCCCTGGCAGACCCAGCTAGCGCTGGAGGAGAAGGGCTGCTGCCAGGAAGGAGACAAACCT
GGCCAAGGAGCTGGAGAGAAGAAGAGGGAGGCCAGCAGCTCAGGATGGAGCTGGCCATCAGAAACCTCAG
CCCTGGACACCTGCATCAAGACCAAGTCGCAGCCGATGATGCCAGTGTCAAGGCCATGGCCCTGTCCCC
```

AACCCCCAGCCCATCGACCCAGCTAGCCTGGAGGAGTTCAAGAGGAAGATCCTGGAGTCCCAGAGGCC TGCAGGCATCCCTGTAGCCCCATCCAGTGGCT <u>GAGGAGGCTCCAGGCCTGAGGACCAAGGGATGGCCCGAC</u> <u>T</u>

The disclosed NOV7b nucleic acid sequence, localized to chromosome 19, has 969 of 1383 bases (70%) identical to a PV-1 mRNA from *Rattus norvegicus* (GENBANK-ID: AF154831) ($E = 2.5e^{-123}$).

- 5 A disclosed NOV7b polypeptide (SEQ ID NO:21) encoded by SEQ ID NO:20 is 442 amino acid residues and is presented using the one-letter amino acid code in Table 7D. Signal P, Psort and/or Hydropathy results predict that NOV7b has a signal peptide and is likely to be localized in the plasma membrane with a certainty of 0.7900. In other embodiments, NOV7b is also likely to be localized to the nucleus with a certainty of 0.6000, to the microbody
- 10 (peroxisome) with a certainty of 0.3000, or the Golgi body with a certainty of 0.3000. The most likely cleavage site for a NOV7b peptide is between amino acids 50 and 51, at: YVG-NV.

Table 7D. Encoded NOV7b protein sequence (SEQ ID NO:21).

MGLAMEYGGSYARAGGSSRGWCYYLRYFFLFVSLIQQFLIIILGLVLFMVYGDHVHVS SQLGLLTASQNLTKELNFTTRAKDAIMQMWLNRARRDLDRINASFRQCQGDRVIYTNNQR YMAAIILSEKQCRDQFKDMNKSCDALLFMLNQKVKTLEVIAKEKTICKDKESVLLNKRV VAEEQLVCEVKTRELQHQERQLAKEQLQKVQALCLPLDKDFEMDLRNLRDSIIPRS LDNLGYNLHYPLGSELASIRRACDHMPSLMSSKVEELARSLSRADIERVARENS DLQRQKLEAQOGLRASQEAKQKVEKEQAAREAKLQAECSRQTOLALEEKAVLR KERDNLAKALEEKKREAEQLRMELAIRNSALDTCKTQSQPMMPSVRPMGPVPNP QPIDPASLEEFKRKILESQRPAPAGIVPAPSSG

- 15 The disclosed NOV7b amino acid sequence has 268 of 442 amino acid residues (60%) identical to, and 350 of 442 amino acid residues (79%) similar to the 438 amino acid residue PV-1 protein from *Rattus norvegicus* (SPTREMBL-ACC:Q9WV78), and 454 of 457 amino acid residues (99%) identical to, and 457 of 457 amino acid residues (100%) similar to the 479 amino acid residue Human ORFX ORF1918 polypeptide sequence (patp:AAB42154) ($E = 1.3e^{-237}$).

20 NOV7b is expressed in at least the following tissues: lymph node, bone marrow, spleen, mammary gland, thyroid, stomach, fetal kidney, heart, fetal liver. In addition, the sequence is predicted to be expressed in lung because of the expression pattern of (GENBANK-ID: Q9WV78) a closely related PV-1 homolog in species *Rattus norvegicus*. It has also been reported to be expressed in muscle and brain (J Cell Biol 1999 Jun 14;145(6):1189-98). Endothelium of the fenestrated peritubular capillaries of the kidney and those of the intestinal villi, pancreas, and adrenals have also been shown to express PV-1 (Proc

Natl Acad Sci U S A 1999 Nov 9;96(23):13203-7) TaqMan data for NOV7b can be found below in Example 2.

NOV7c

5 A disclosed NOV7c nucleic acid of 2024 nucleotides (also referred to CG51878-03) encoding a novel PV-1-like receptor protein is shown in Table 7E. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TGA codon at nucleotides 1327-1329. In Table 7E, the 3' untranslated region is underlined and the start and stop codons are in bold letters.

10

Table 7A. NOV7c Nucleotide Sequence (SEQ ID NO:22)

```

ATGGGTCTGCCATGGAGCACGGAGGGTCCTACGCTCGGGGGGGCAGCTCTGGGGCTGCTGGTATTA
CCTCGCTACTTCTCTCGTCCCTCATCCAATTCTCATCCTCGGGCTCGTGTCTTCATGG
TCTATGGCAACGTGCACTGAGCACAGAGTCCAACCTGCAAGGCCACCGAGCGGGAGGGCTATAC
AGTCAGCTCTAGGGCTACGGCCTCCAGTCCAACTTGACCAAGGAGCTCAATTCAACCACCGGCCAA
GGATGCCATCATGCAAGATGTGGCTGAATGCTCGTCCGACCTGGAGCGCATCAATGCCAGCTCCGCGAGT
GCCAGGGTGACCGGGTCACTCACAGAACACAATCAGAGGTACATGGCTGCCATCATCTTGAGATGAGAACAA
TGCAGAGATCAATTCAAGGACATGAACAAAGAGCTGCCATGGCTCTTCATGCTGAATCAGAAAGGTGAA
GACGCTGGAGGTGGAGATGCCAAGGAGAACAGCTGGTGAATGCGTGAACACCCGGAGCTGCAGCACCAAGAGCGCCAGCTG
GCCAAGGAGCAACTGCAAAGGGTCAAGGCCCTGCGCTGCCCCCTGGACAAGGACAAGTTGAGATGGACCT
TCGTAACCTGTGGAGGGACTCCATTATCCCACTGCCAGCAGCTGGACAACCTGGGTTACAACCTCTACCATCCCC
TGGGCTGGAAATTGGCTCATGCCAGACGGCTGGCACACATGCCAGCTCGTGAAGCTCCAAGGTGGAG
GAGCTGGCCGGAGGCTCCGGGCGATACTGAACCGCTGGCCGGAGACTCAGACCTCAACGCCAGAA
GCTGGAAAGCCCAGCAGGGCTCGGGCCAGTCAGGAGCCGAAACAGAAAGGTGGAGAAGGGCTCAGGCC
GGGAGGAGCAAGCTCAAGCTGAATGCTCCGGCAGACCCAGCTAGCGCTGGAGGGAGAGCGGTGCTGCGG
AAGGAACGAGACAACCTGGCAAGGAGCTGGAGAAGAACAGAGGGAGGGAGAGCTCAGGAATGGAGCT
GGCCATCAGAAACTCAGCCTGACACTGCTCATCAAGAACACAAGTCCAGCCAGTGAAGCTGCAAGG
CCATGGGCCCTGTCCCCAACCCCAGGCCATGCCAGCTAGGCTGAGGAGTTCAAGAGGAAGATCCCTG
GAGTCCCAGAGGCCCTGTGAGGCATCCCTGTAGGCCCCTGCCAGTGGCTGAGGAGCTCAGGCCAGGA
CCAAGGGATGGCCGACTCGGCGTTTGGCAGGATGCCAGGGATATGCTCACAGGCCAGAACACCCCC
TCCCGCCGCCAACACCAGGGCACCATCAGACAACCTCCCTGATGCCAAACCCCTAGTACCCCTCA
CACCCGACCCGCCCTCATGATCCCTCACCGAGAACACAGCCGGAGATGACGTCACGCAAGCAACG
GCGCTGACGTCACATATCACCGTGTGATGGCTCACGTGGCCATGTAGACGTCAGGAAGAGATATAGCGA
TGGCGTGTGCAAGTGCAGCACTGCGCACACAGACATGGGAACTTGGCATGCTCACCGAGATGCGAG
CAACGACGTCACGGGCCATGTGAGCTCACACATATTATGTCACACAGACAGCGGGATGGCATCACACAG
ACGGTGTGATGTCACACACAGACACAGTGAACACACACCATGACAACGACACCTATAGATATGGCACC
AACATCACATGCAAGCATGCCCTTACACACACACTTCTACCCAATTCTCACCTAGTGTCACTGTTCCCCCG
ACCCCTGGCACACGGGCCAGGTACCCACAGGATCCCATCCCCCTCCGCACAGGCCCTGGGCCCCACCTC
CCCTCCCTGAGCCCTGTGGCTCCCGTAGTACACAG

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The disclosed NOV7c nucleic acid sequence, localized to chromosome 19p13, has 2009 of 2015 bases (99%) identical to a gb:GENBANK-ID:AF326591|acc:AF326591.1 mRNA from *Homo sapiens* (*Homo sapiens* fenestrated-endothelial linked structure protein 15 (FELS) mRNA, complete cds) (E =0.0).

A disclosed NOV7c polypeptide (SEQ ID NO:23) encoded by SEQ ID NO:22 is 442 amino acid residues and is presented using the one-letter amino acid code in Table 7F. Signal P, Psort and/or Hydropathy results predict that NOV7c has a signal peptide and is likely to be

localized in the plasma membrane with a certainty of 0.7900. In other embodiments, NOV7c is also likely to be localized to the nucleus with a certainty of 0.6000, to the microbody (peroxisome) with a certainty of 0.3000, or the Golgi body with a certainty of 0.3000. The most likely cleavage site for a NOV7c peptide is between amino acids 50 and 51, at: YVG-
5 NV.

Table 7F. Encoded NOV7c protein sequence (SEQ ID NO:23).

MGLAMEHGGSYARAGGSRGWCYIILRYFFLFVSLIQFLIIILGLVLFMVYGNVHVSTESNLQATERRAEGLY
SQLLGLTASQSNLTKELMFTTRAKDAIMQMWNLNARRDLDNRINASFRQCQGDVRIVYTNNQRYMAAIILSEKQ
CRDQFKDMNKSCDALLFBLNQPKVKTLTEVEIAKEKTCTIKDKESVLLNKRVAEQLVECVKTRELQHQERQL
AKEBOLQRVOALCLPLDKDFEMDLRNLRDTSIIPRSIDLNLGYLYHPLGSELASIRRACDHMPSLVSSKVE
ELARSLRADIERVARENDSLQRQKLEAQOGLRASQEAKQKVEKEAQAREAKLQAECCSRQTQLALEEKAVLR
KERDNLAKLEEEKKREABQLRMELAIRNSALDTCTIKTSQPMMPVSRPMGPVPNQPQIDPASLEEFKRKIL
ESORPPAGIPVAPSSG

The disclosed NOV7c amino acid sequence has 440 of 442 amino acid residues (99%) identical to, and 442 of 442 amino acid residues (100%) similar to, the 442 amino acid residue ptnr:SPTREMBL-ACC:Q9BX97 protein from *Homo sapiens* (Human) (PV1 PROTEIN) (E = 6.9e⁻²³¹).

NOV7c is expressed in at least the following tissues: Heart, Adrenal Gland/Suprarenal gland, Thyroid, Salivary Glands, Liver, Bone Marrow, Spleen, Lymph Node, Mammary gland/Breast, Placenta, Prostate, Lung, Kidney, Pancreas, Bone Marrow, and Small Intestine.

15 Expression information was derived from the tissue sources of the sequences that were included in the derivation of the sequence of CuraGen Acc. No. CG51878-03. The sequence is predicted to be expressed in the following tissues because of the expression pattern of (GENBANK-ID: gb:GENBANK-ID:AF326591|acc:AF326591.1) a closely related *Homo sapiens* fenestrated-endothelial linked structure protein (FELS) mRNA.

20 The NOV7a, 7c and 7c are very closely homologous as is shown in the alignment in
Table 7G.

Table 7G Alignment of NOV7a, 7b, and 7c.

		130	140	150	160	170	180	
5	NOV7a	GDRVIYTNNQRYMAAIILSEKQCRDQFKDMNKSCDALLFMLNQKVKTLEVEIAKEKTICT						180
	NOV7b	GDRVIYTNNQRYMAAIILSEKQCRDQFKDMNKSCDALLFMLNQKVKTLEVEIAKEKTICT						180
	NOV7c	GDRVIYTNNQRYMAAIILSEKQCRDQFKDMNKSCDALLFMLNQKVKTLEVEIAKEKTICT						180
		190	200	210	220	230	240	
10	NOV7a	KDKESVLLNKRVAEEQLVECVKTRLEQHQERQLAKEQLOQKVQALCLPLDKDKFEMDLRNL						240
	NOV7b	KDKESVLLNKRVAEEQLVECVKTRLEQHQERQLAKEQLOQKVQALCLPLDKDKFEMDLRNL						240
	NOV7c	KDKESVLLNKRVAEEQLVECVKTRLEQHQERQLAKEQLOQKVQALCLPLDKDKFEMDLRNL						240
		250	260	270	280	290	300	
15	NOV7a	WRDSIIPRSLDNLGYNLYHPLGSELASIRRACDHMPSLMSSKVE <u>EO</u> CRSLRADIERVARE						300
	NOV7b	WRDSIIPRSLDNLGYNLYHPLGSELASIRRACDHMPSLMSSKVE <u>EEL</u> ARSLRADIERVARE						300
	NOV7c	WRDSIIPRSLDNLGYNLYHPLGSELASIRRACDHMP <u>SLV</u> SSKVEEELARSLRADIERVARE						300
		310	320	330	340	350	360	
20	NOV7a	NSDLQRQKLEAQQQGLRASQEAKQKVKEAQAREAKLQAECCSRQTQLALEEKAVLRKERDN						360
	NOV7b	NSDLQRQKLEAQQQGLRASQEAKQKVKEAQAREAKLQAECCSRQTQLALEEKAVLRKERDN						360
	NOV7c	NSDLQRQKLEAQQQGLRASQEAKQKVKEAQAREAKLQAECCSRQTQLALEEKAVLRKERDN						360
		370	380	390	400	410	420	
25	NOV7a	LAKELEEKKREAEQLRMLELAIRNSALDT <u>CI</u> TKSQPNMPVSRPMGPVPNPQPIDPASLEE						420
	NOV7b	LAKELEEKKREAEQLRMLELAIRNSALDT <u>CI</u> TKSQPNMPVSRPMGPVPNPQPIDPASLEE						420
	NOV7c	LAKELEEKKREAEQLRMLELAIRNSALDT <u>CI</u> TKSQPNMPVSRPMGPVPNPQPIDPASLEE						420
		430	440					
35	NOV7a	FKRKILESQRPPAGIPVAPSSG 442 (SEQ ID NO:19)						
	NOV7b	FKRKILESQRPPAGIPVAPSSG 442 (SEQ ID NO:21)						
	NOV7c	FKRKILESQRPPAGIPVAPSSG 442 (SEQ ID NO:23)						

Homologies to any of the above NOV7 proteins will be shared by the other two NOV7 proteins insofar as they are homologous to each other as shown above. Any reference to NOV7 is assumed to refer to all three of the NOV7 proteins in general, unless otherwise noted.

NOV7a also has homology to the amino acid sequence shown in the BLASTP data listed in Table 7H.

Table 7H. BLAST results for NOV7a

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 12963353 gb AAK11 226.1	fenestrated- endothelial linked structure protein [Homo sapiens]	442	438/442 (99%)	438/442 (99%)	0.0
gi 13775238 ref NP_1 12600.1	fenestrated- endothelial linked structure protein; PV-1 protein [Homo sapiens])	442	439/442 (99%)	439/442 (99%)	0.0
gi 9910520 ref NP_06 4471.1	PV-1 [Rattus norvegicus]	438	266/442 (60%)	347/442 (78%)	e-131
gi 14161394 gb AAK54 730.1 AF369900.1	MECA32 [Mus musculus]	438	270/442 (61%)	348/442 (78%)	e-125

gi 14161698 ref NP_1 15774.1	plasmalemma vesicle associated protein [Mus musculus]	438	269/442 (60%)	346/442 (77%)	e-125
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The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 7I.

Table 7I. Information for the ClustalW proteins

- 5 1) NOV7 (SEQ ID NO:19)
 2) gi|12963353|gb|AAK11226.1| fenestrated-endothelial linked structure protein
 [Homo sapiens] (SEQ ID NO:55)
 3) gi|13775238|ref|NP_112600.1| fenestrated-endothelial linked structure protein;
 PV-1 protein [Homo sapiens]) (SEQ ID NO:56)
10 4) gi|9910520|ref|NP_064471.1| PV-1 [Rattus norvegicus] (SEQ ID NO:57)
 5) gi|14161394|gb|AAK54730.1|AF369900_1 MECA32 [Mus musculus] (SEQ ID NO:58)
 6) gi|14161698|ref|NP_115774.1| plasmalemma vesicle associated protein [Mus
 musculus] (SEQ ID NO:59)

		10	20	30	40	50
15	NOV7
	gi 12963353	MGLAMEHGGSYARACGSSRGCWYIYLRYFFLTVSLIQQLFLII	LGLVLVFMIVG			
	gi 13775238	MGLAMEHGGSYARACGSSRGCWYIYLRYFFLTVSLIQQLFLII	LGLVLVFMIVG			
20	gi 9910520	MGLAMEHGGSYARACGSSRGCWYIYLRYFFLTVSLIQQLFLII	LGLVLVFMIVG			
	gi 14161394	MGLSMDRS-PYARTGDDQRCGCWYIYLRYFFLTVSLIQQLFLII	LGLVLVFMIVG			
	gi 14161698	MGLSMDRS-PYARTGDDQRCGCWYIYLRYFFLTVSLIQQLFLII	LGLVLVFMIVG			
25	NOV7
	gi 12963353	NVHVSTESTNLGATERRAEGLYSQQLGLTASQNLTKELNFITTRAKDAMQ				
	gi 13775238	NVHVSTESTNLGATERRAEGLYSQQLGLTASQNLTKELNFITTRAKDAMQ				
30	gi 9910520	NVHVSTESTNLGATERRAEGLYSQQLGLTASQNLTKELNFITTRAKDAMQ				
	gi 14161394	NVHVATTESSLRATEIRADNLSSQVGLSAAQNLSKOLNISTLVKDTIYMQ				
	gi 14161698	NVHVATTESSLRATEIRADNLSSQVGLSAAQNLSKOLNISTLVKDTIYMQ				
35	NOV7
	gi 12963353	MWLNRARRDIDRINASFRQCQGDRLVITYTNNORNYMAAIIILSEKQCRCDFKDM				
	gi 13775238	MWLNRARRDIDRINASFRQCQGDRLVITYTNNORNYMAAIIILSEKQCRCDFKDM				
	gi 9910520	MWLNRARRDIDRINASFRQCQGDRLVITYTNNORNYMAAIIILSEKQCRCDFKDM				
40	gi 14161394	QLLTTRREVERINASFRQCQGDRLVITYINYNRFIAAIIILSEKQCQEQDLKEG				
	gi 14161698	QLLTTRREVERINASFRQCQGDRLVITYINYNRFIAAIIILSEKQCQEQDLKEG				
45	NOV7
	gi 12963353	NKSCDALLFMLNQOKVKITLEVEVIAKEKTIICKDKDESILLNKRVVAEEQQLVEC				
	gi 13775238	NKSCDALLFMLNQOKVKITLEVEVIAKEKTIICKDKDESILLNKRVVAEEQQLVEC				
	gi 9910520	NKSCDALLFMLNQOKVKITLEVEVIAKEKTIICKDKDESILLNKRVVAEEQQLVEC				
50	gi 14161394	NKTCCEALLFKLGKVKITLEMEVIAKEKAVCSKDKDESILLAKRQAEQEC				
	gi 14161698	NKTCCEALLFKLGKVKITLEMEVIAKEKAVCSKDKDESILLAKRQTEEQLEAC				
55	NOV7
	gi 12963353	VKTIRELQHQEROFIAKEOLOKVRQLCPLDKDFEMDLNNLWRDSIIPRSL				
	gi 13775238	VKTIRELQHQEROFIAKEOLOKVRQLCPLDKDFEMDLNNLWRDSIIPRSL				
	gi 9910520	VKTIRELQHQEROFIAKEOLOKVRQLCPLDKDFEMDLNNLWRDSIIPRSL				
	gi 14161394	GKARERQQEQCQWVPEENLRKVQSLCPLDKFQADWLSAWRDSDIHYRTL				
	gi 14161698	GKARERQQEQCQWVPEENLRKVQSLCPLDKFQADWLSAWRDSDIHYRTL				

		260	270	280	290	300	
	NOV7	
5	gi 12963353	DNLGYNLYXPILGSELASIRRACDIMPSSKVEGQCRSLRADIERVARE	DNLGYNLYXPILGSELASIRRACDIMPSSKVEELARSLRADIERVARE				
	gi 13775238	DNLGYNLYXPILGSELASIRRACDIMPSSKVEELARSLRADIERVARE	DNLGYNLYXPILGSELASIRRACDIMPSSKVEELARSLRADIERVARE				
	gi 9910520	DNLGY--HMSLMPEFSSURRTCESLPGIMTKVEELARGLRAGIERVTRE	DNLGY--HMSLMPEFSSURRTCESLPGIMTKVEELARGLRAGIERVTRE				
	gi 14161394	EILPY--HYQLMPEYASIRRRTCESLPGIMTKIEELARGLRAGIERVTRE	EILPY--HYQLMPEYASIRRRTCESLPGIMTPKIEEWARGVRAGIERVTRE				
	gi 14161698	EILPY--HYQLMPEYASIRRRTCESLPGIMPPKIEEWARGVRAGIERVTRE	EILPY--HYQLMPEYASIRRRTCESLPGIMPPKIEEWARGVRAGIERVTRE				
10		310	320	330	340	350
	NOV7	NSDLQRQKLEAQOGLRASQEAKQKVEKEAQAREAKLCAECSRQTQLALEE	NSDLQRQKLEAQOGLRASQEAKQKVEKEAQAREAKLCAECSRQTQLALEE				
	gi 12963353	NSDLQRQKLEAQOGLRASQEAKQKVEKEAQAREAKLCAECSRQTQLALEE	NSDLQRQKLEAQOGLRASQEAKQKVEKEAQAREAKLCAECSRQTQLALEE				
15	gi 13775238	NSDLQRQKLEAQOGLRASQEAKQKVEKEAQAREAKLCAECSRQTQLALEE	NSDLQRQKLEAQOGLRASQEAKQKVEKEAQAREAKLCAECSRQTQLALEE				
	gi 9910520	NGELRRQKLELERATQCEREARTRAGTEAQARETOLRAECARQTQLALEE	NAELRRQKLELERAAQAEQARAGTEAQARETOLRAECARQTQLALEE				
	gi 14161394	NAELRRQKLELERAAQAEQARAGTEAQARETOLRAECARQTQLALEE	NAELRRQKLELERAAQAEQARAGTEAQARETOLRAECARQTQLALEE				
	gi 14161698	NAELRRQKLELERAAQAEQARAGTEAQARETOLRAECARQTQLALEE	NAELRRQKLELERAAQAEQARAGTEAQARETOLRAECARQTQLALEE				
20		360	370	380	390	400
	NOV7	KAVLRKGDRDNLAKELEEKKREAEQLRMEIAIRNSALDTCKTKSQEMMPV	KAVLRKGDRDNLAKELEEKKREAEQLRMEIAIRNSALDTCKTKSQEMMPV				
	gi 12963353	KAVLRKGDRDNLAKELEEKKREAEQLRMEIAIRNSALDTCKTKSQEMMPV	KAVLRKGDRDNLAKELEEKKREAEQLRMEIAIRNSALDTCKTKSQEMMPV				
25	gi 13775238	KAALRIGDLDLEROLEARKRELEQLRTEVIDVRIISALDTCVKAKSLEAVPP	KAALRIGDLDLEROLEARKRELEQLRTEVIDVRIISALDTCVKAKSLEAVPP				
	gi 9910520	KAALRIGDLDLEROLEARKRELEQLRTEVIDVRIISALDTCVKAKSLEAVPP	KAALRIGDLDLEROLEARKRELEQLRTEVIDVRIISALDTCVKAKSLEAVPP				
	gi 14161394	KAALRIGDLDLEROLEARKRELEQLRTEVIDVRIISALDTCVKAKSLEAVPP	KAALRIGDLDLEROLEARKRELEQLRTEVIDVRIISALDTCVKAKSLEAVPP				
	gi 14161698	KAALRIGDLDLEROLEARKRELEQLRTEVIDVRIISALDTCVKAKSLEAVPP	KAALRIGDLDLEROLEARKRELEQLRTEVIDVRIISALDTCVKAKSLEAVPP				
30		410	420	430	440	
	NOV7	SRPMGEVPNPQPIDPASLEEFKKRILESRQRPPAGIPVAPSSG	SRPMGPVDPNPQPIDPASLEEFKKRILESRQRPPAGIPVAPSSG				
	gi 12963353	SRPMGPVDPNPQPIDPASLEEFKKRILESRQRPPAGIPVAPSSG	SRPMGPVDPNPQPIDPASLEEFKKRILESRQRPPAGIPVAPSSG				
	gi 13775238	-RLPGPPPNNPPIPDPASLEEFKKRILESRQRPLVLNPVAPPPSG	-RVSGPPPNNPPIPDPASLEEFKKRILESRQRPLVVNPAPQPSG				
35	gi 9910520	-RLPGPPPNNPPIPDPASLEEFKKRILESRQRPLVLNPVAPPPSG	-RVSGPPPNNPPIPDPASLEEFKKRILESRQRPLVVNPAPQPSG				
	gi 14161394	-RVSGPPPNNPPIPDPASLEEFKKRILESRQRPLVVNPAPQPSG	-RVSGPPPNNPPIPDPASLEEFKKRILESRQRPLVVNPAPQPSG				
	gi 14161698	-RVSGPPPNNPPIPDPASLEEFKKRILESRQRPLVVNPAPQPSG	-RVSGPPPNNPPIPDPASLEEFKKRILESRQRPLVVNPAPQPSG				

PV-1 is a novel endothelial protein shown by immunocytochemical tests to be specifically associated with the stomatal diaphragms of caveolae in lung endothelium (Stan RV, et.al.; Proc Natl Acad Sci U S A 1999 Nov 9;96(23):13203-7). Although the highest expression levels of both mRNA and protein are in the lung, PV-1 also has been found to be expressed in other organs. Using a specific antibody to the extracellular domain of PV-1, the survey on the presence of this protein at light and electron microscope level has been extended in several rat organs. It has been shown by immunofluorescence the antibody recognizes with high specificity the endothelium of the fenestrated peritubular capillaries of the kidney and those of the intestinal villi, pancreas, and adrenals. By immunolocalization at electron microscope level, the antibody recognizes specifically the diaphragms of the fenestrae and the stomatal diaphragms of caveolae and transendothelial channels in the endothelia of these vascular beds. No signal was detected in the continuous endothelium of the heart, skeletal muscle, intestinal muscularis, or brain capillaries or the non-diaphragmed fenestrated endothelium of kidney glomeruli. Taken together, the findings define the only antigen to be localized thus far in fenestral diaphragms. They also show that the stomatal diaphragms of

caveolae and transendothelial channels and the fenestral diaphragms might be biochemically related, in addition to being morphologically similar structures.

By using an immunoisolation procedure (Stan, R.-V., W.G. Roberts, K. Ihida, D. Predescu, L., Saucan, L. Ghitescu, and G.E. Palade. 1997. Mol. Biol. Cell. 8:595-605)

5 developed in our laboratory, a caveolar subfraction from rat lung endothelium has been isolated and the proteins of this subfraction have been partially characterized which include an apparently caveolae-specific glycoprotein proposed to be called PV-1 (formerly known as gp68). The isolation and partial sequencing of PV-1, combined with the cloning of the full length PV-1 cDNA led to the following conclusions: (a) PV-1 is a novel single span type II integral membrane protein (438 amino acids long) which forms homodimers in situ; (b) the transmembrane domain of PV-1 is near the NH₂ terminus defining a short cytoplasmic endodomain and a large COOH-terminal ectodomain exposed to the blood plasma; (c) PV-1 is N-glycosylated and its glycan antennae bear terminal nonreducing galactosyl residues in alpha1-3 linkage. PV-1 is expressed mostly in the lung but both the messenger RNA and the protein can be detected at lower levels also in kidney, spleen, liver, heart, muscle, and brain.

10 No signal could be detected in testis and two lower molecular weight forms were detected in brain. Immunocytochemical studies carried out by immunodiffusion on rat lung with an anti-PV-1 polyclonal antibody directed against a COOH-terminal epitope reveal a specific localization of PV-1 to the stomatal diaphragms of rat lung endothelial caveolae and confirm the extracellular orientation of the PV-1 COOH terminus (Stan, R.V. J. Cell. Biol. 1999, Jun. 14; 145(6): 189-98).

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Immunohistochemistry revealed initial expression of the stage-specific glycoprotein, GP68, in various mesenchymal tissue substructures of mouse embryos (Morita T, et.al.; Okajimas Folia Anat Jpn 1998 Oct;75(4):185-95). During the 11-15th days of gestation, GP68 was localized in the primitive meninges, chondroblasts and perichondrium of pre-cartilaginous vertebral bodies and ribs, connective tissue cells of the dermis, the epicardium and endocardium of the heart, the epimysium and perimysium of skeleton musclature, and the basement membranes of splanchnic organs. Double staining for laminin expression indicated coincidental expression in identical tissue substructures. However, laminin was expressed in days 10-18 embryos and the neonate. Therefore, GP68 is coincidentally expressed with laminin in mesenchymal tissues between the 11th and 15th day of gestation, and may play a role as a laminin-associated protein. In the light of these results, a hypothesis concerning the relationship between these two proteins and the mechanisms of non-integrin laminin-associated proteins during normal embryogenesis is discussed further.

The microvascular endothelium is organized as a highly differentiated squamous epithelium whose main function is to mediate the exchanges of water, macromolecules, and small solutes between the blood plasma and the interstitial fluid. The endothelial structures implicated so far in the transendothelial transport are the caveolae, transendothelial channels, 5 intercellular junctions, and the fenestrae. Caveolae are flask-shaped or spherical plasma membrane invaginations and associated vesicles of 70-nm average outer diameter that can occur singly or in chains or clusters. In invaginated form, their membranes are in continuity layer by layer with the plasmalemma proper, and, in some microvascular beds (e.g., the continuous endothelium of the lung and the fenestrated and sinusoidal endothelia), their 10 introits or necks are provided with a stomatal diaphragm.

The transendothelial channels are channels of 60-70-nm diameter that run across the endothelial cell. They seem to be formed by the fusion of either one caveola with both luminal and abluminal aspects of the plasmalemma or by chains of usually two to four caveolae. These channels are provided with two diaphragms (one luminal and one abluminal) only in 15 fenestrated endothelia and not in their continuous counterparts.

The diaphragmed fenestrae are characteristic structural elements of all fenestrated endothelia (e.g., kidney peritubular capillaries and ascending vasa recta, capillaries of intestinal villi, pancreas, adrenal cortex, endocrine glands, and choriocapillaries of the brain and eye). They are round openings or windows cutting through the endothelial cell, have a 20 constant diameter of 63-68 nm, and occur only in the attenuated parts of the cell, in clusters referred to as "sieve plates". In en face electron microscopic images, the fenestrae appear circular, but several studies have shown that they have an 8-fold symmetry. The rim of the fenestra (where the abluminal plasmalemma is continuing the luminal plasmalemma) is the anchoring line for the fenestral diaphragm. In normal sections, the diaphragm appears as a 25 very thin (5-6 nm) single-layer barrier provided with a central density or knob. Deep-etch rapid-freeze techniques have revealed the structure of the diaphragm to be composed of radial fibrils (7-nm diameter) starting at the rim and interweaving in a central mesh (the equivalent of the central knob in orthogonal sections).

Although the chemical composition of endothelial caveolae started to yield some 30 insights, the molecular components of transendothelial channels and fenestrae remained elusive. The chemistry of these endothelial microdomains has been investigated with nonspecific "general" probes (charged molecules and lectins alone or in combination with various degrading enzymes), which yielded some information on the surface charge, type of molecules conferring the charge, and type of glycan antennae found on the glycoproteins and

glycolipids. No specific component of the fenestral or transendothelial channels diaphragms has been identified so far.

Proteins reported to be contained within caveolae include G protein-coupled receptors (GPCR) (Ostrom RS , et al., J Pharmacol Exp Ther 2000 Aug;294(2):407-12), scavenger receptor class B type I (SR-BI) (Krieger M Annu Rev Biochem 1999;68:523-58), Monocarboxylate transporters (Bonen A, Med Sci Sports Exerc 2000 Apr;32(4):778-89), endothelial NOS (eNOS) (Kone BC Acta Physiol Scand 2000 Jan;168(1):27-31). IP3 receptor-like protein, Ca²⁺ ATPase, several PKC isoforms. (Isshiki M, et al., Cell Calcium 1999 Nov;26(5):201-8). and GPI-anchored molecules (Martins VR, Braz J Med Biol Res 1999 Jul;32(7):853-9).

The disclosed NOV7 nucleic acid of the invention encoding a PV-1 -like protein includes the nucleic acid whose sequence is provided in Table 7A, 7C, or 7E or a fragment thereof. The invention also includes a mutant or variant nucleic acid any of whose bases may be changed from the corresponding base shown in Table 7A, 7C, or 7E while still encoding a protein that maintains its PV-1 -like activities and physiological functions, or a fragment of such a nucleic acid. The invention further includes nucleic acids whose sequences are complementary to those just described, including nucleic acid fragments that are complementary to any of the nucleic acids just described. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications. Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject. In the mutant or variant nucleic acids, and their complements, up to about 30% percent of the bases may be so changed.

The disclosed NOV7 protein of the invention includes the PV-1 -like protein whose sequence is provided in Table 7B, 7D, or 7F. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in Table 7B, 7D, or 7F while still encoding a protein that maintains its PV-1 -like activities and physiological functions, or a functional fragment thereof. In the mutant or variant protein, up to about 40% percent of the residues may be so changed.

The protein similarity information, expression pattern, and map location for the PV-1-like protein and nucleic acid (NOV7) disclosed herein suggest that NOV7 may have important structural and/or physiological functions characteristic of the PV-1-like family. Therefore, the

NOV7 nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications. These include serving as a specific or selective nucleic acid or protein diagnostic and/or prognostic marker, wherein the presence or amount of the nucleic acid or the protein are to be assessed, as well as potential therapeutic applications such as the
5 following: (i) a protein therapeutic, (ii) a small molecule drug target, (iii) an antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) a nucleic acid useful in gene therapy(gene delivery/gene ablation), and (v) a composition promoting tissue regeneration in vitro and in vivo.

The NOV7 nucleic acids and proteins of the invention are useful in potential diagnostic
10 and therapeutic applications implicated in various diseases and disorders described below and/or other pathologies. For example, the compositions of the present invention will have efficacy for treatment of patients suffering from Cerebellar ataxia, pure; Episodic ataxia, type 2; Hemiplegic migraine, familial; Leigh syndrome; Spinocerebellar ataxia-6; Psoriasis, susceptibility to; Autoimmune disease, Asthma, Emphysema, Scleroderma, allergy, ARDS,
15 Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Muscular dystrophy, Myasthenia gravis, Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies,
20 Graft vesus host, Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation, Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Scleroderma, Obesity, Transplantation; fertility; cancer; Renal artery stenosis, Interstitial nephritis,
25 Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalceimia, Lesch-Nyhan syndrome, Adrenoleukodystrophy, Congenital Adrenal Hyperplasia, Xerostomia; tooth decay and other dental problems; Inflammatory bowel disease, Diverticular disease, Pancreatitis, and/or other pathologies/disorders. The NOV7 nucleic acid, or fragments thereof, may further be useful in
30 diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

NOV7 nucleic acids and polypeptides are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the

art, using prediction from hydrophobicity charts, as described in the "Anti-NOVX Antibodies" section below. For example the disclosed NOV7 protein have multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, contemplated NOV7 epitope is from about amino acids 5 to 25. In other embodiments, NOV7 epitope is from 5 about amino acids 50 to 75, from about amino acids 80 to 160, from about amino acids 175 to 275, from about amino acids 280 to 380, or from about amino acids 385 to 430. This novel protein also has value in development of powerful assay system for functional analysis of various human disorders, which will help in understanding of pathology of the disease and development of new drug targets for various disorders.

10

NOV8

NOV8 includes two novel Papin-like proteins disclosed below. The disclosed proteins have been named NOV8a, and NOV8b.

NOV8a

15 A disclosed NOV8a nucleic acid of 8640 nucleotides (also referred to as SC134914330_A) encoding a novel papin-like protein is shown in Table 8A. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 101-103 and ending with a TGA codon at nucleotides 8543-8545. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 20 8A. The start and stop codons are in bold letters.

Table 8A. NOV8a nucleotide sequence (SEQ ID NO:24).

AGCTGATGATGGCCAGGGACCCCAGGGGACGTGGGGCCCTGTGGGGTCTGGCCCCCAGGAGCAAGACCTCTG ATGATGCTGGTGTCTGGGAGTGAGCACCATGCCCATC AACCCAGGACAATGCCGTGCTGCACCTGCCCTCCT CTAACCGAGCTGCAGAACAGCCTGCAGGAAGGTGGGATGGGCCGAGCAGGGCTCTGCCAGGGCGCCAT CCAGAACGGCTCAGGAGTACATCCAGCTGAACATTGCTGTGGATGAGAGTACGGTCCCACCTGTACACAGCCC CCCCGAAATGGAGATCTGTACTGTGTACCTCACCAAGGAGCTGGGGACACAGAGACTGTGGGCTGAGTT TGGAAATCCTCTGTTTCGGGGATATGGTAAAGGGCAGGGGGGCAAGAAGGAAAACCCACCAGGG TCTCTGCTGGATGTGGCTGACCTGGAGCTGAGGAGCTGAGGAAGAACAGCCCAGCAGGGAGAGTGGGA GGTCCGACTCGGGGATGAGATCCTCTACTGAATGGCGAGCTGATGGTTGGAGGTTGATGTCAGTGGGCCAG TTACCTGGCTGAGCACTCTGGAAATGGCGGTTTATCTACCTGTACATGCTGCGCTGCTTTAACGACAAAGC CCACTCCACTATAATGGAACAGTAGAACAGCTCTGAACCAGGGAGAAACACCTACCTTGGAGCTGGGTGA CCGAACTGCGAAAAGGGGAAACGAAACCAGAAGTTGGGTCTCTCCAGGCCCTGCCCACAAAGGCC TGAAGAAATCCAAGGGCAGCGCTGGCTGTGAGCTGCTGGAGCTGACCTGGAGCTGGAGAACGGCCCTGGA CCCTGAACCTGGAAACGGCCATGTCTTCAGCTAGAAAATGGGCCGAGATTCTCTCAAGGAGGTGGCTGGACC CCATCTAGAGGGTCAAGAGTGGACAGAGGGACAGAGCATAGAATTCAAAGACAGATGCTCTCTGACCAC AAGCAATGACAAACGCCCTCTCAAAGGTGGAGACGGACTTCAATCGAGTGACTGCCCTGGCACGGTC CAAGGAGGAAGTTGGCGAATATGGAGATGGAGCTGCTCAAAGAATGGATGGCTGGGAATTCAGGTTAG TGGAGGCCAGGGATCAAAGCGCTCACCTCACGCTATCGTTGTCAGTCAAGTGAAGGAAGGAGGTGCCGCTCA CAGGCTCAGGGATGGCAGGCTGTCCTTAGGGAGATGAGCTGCTGGTAATCAATGGTCATTACTGGTCGGGCT CTCCCAAGGGAGCAAGCTGGCCATTCTCGCTCGCCACGGGAATGGTGCAGCTGTGGTGGGAGCAAGGT AGGTGTGCTTCTGCATTCAGATGCTGGGACAGATGAACCCCAAGATGTGTCGGTGTGAGGAATCCAA GGGAACCTGGAAAGTCCAAACAGGGCAGCAATAAAATCAAGCTAAGGAGTCGCCCTTCAGGTAGGTGGGG GCTCTACCTGATGCAGGCTGTGGGGGTGACACGGCCTGAGTCAGTTGAAGAATATAACGAGCTGATGGT

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AGCCATTAGAAAGGCAGAACTCCACGGAAAATCAAGCCTGATGTCAAGACTCCGAGGGGTGCCAGAAA
CAGCATCCAGGGGCCCTCGGGGAGGACCATCTACTTCACCCCAAGGCAGCCACCAGGACTACTC
CATGCCAGCCCGATTCAGCCATTGGACGGGAGGGTCACCCCCCACACAGCCTGGCTCTCGGG
CAGCCAGGTCCCCTGTGACAAGCAGTGTGCTCCCAGGCAAAAGGCATCAGAGGTGCTTCCAGCCTGGC
TAATGCAAGGGCATATACTGTAAGGCGCTGGACACATCGAGGAATCTCCAGCCAAGATGAAGG
GGATATCTTCAGTCAGGAGACGAGCTGCTAGTCACAGACAAAATCAAAGTCACCAGACGACACTACTG
CTATGAGCAGAAGTGGCCCATGAATCTACCTCATTTCTCTGTGAAAGCAGGGATCAAGTCTTGAGAA
CTTGGCCATGCTGACCGGCTGTAGCCAAGTCCGGGCTTCCCATTGGCTGGTGAGCTCAAGCCTCC
CATTGGGAGGCGCTTCGGCAGCATTGTTCCGGAGGCTGGCCACCCAGGTGACGCAGCAGCAAGGTT
GTTGACACGCTGAGTCTGACCGAAAACAAAGGAAGCCGCCACCTCTGCCCCAGATGGCAA
GTCTCCCTCAATCATGAACTGACCATCTCGGAGAACCCACAGAGACAGTAGCAAGGGCTCTGATTC
GGAACATAAGAAATCACTGGCTTGGAAATTCCACCCAAACGATGACCCCTGGCTCTGTTAAAGAG
GAACAGTCCTCGGTACGCCACACGAGCCCTCGCCCGTGTCCGCTCCAAGCTCCAGGAGCTGAGAGCCTT
GAGCATGCTGACCTGACAAGCTCTGAGCGAGGATTACTCAGCAGGGCCAGGCCGTGCTTCAAAAC
TGAGCTGGAGATCACCCAGGAGGTACACCTGGCCCTCTGCTGGAGGCTTCTGCTCCGAGAAGGGCGG
GAACAGGCCCTGCCAGGAGCTGGCCCTAAACACAGTCTGCTGAGACACCCAGTCAGCCAGTGATAC
GGGTGAAGCTGGCCAGGATCTGCTTAAAGAAGCTGGTCAAGTAACTGGATCAACTTCTAGTCTCAGC
GGGGACCCAGAAAGATTACAGTCAGTGTGTTATCGTCAGTGGGATCGAAATCTACCATCTCACTCTCATCA
GGAACCGAAAGCACAACTCAGAGAATGAGAAGATGTTGCTTCAGTCTGAATGAAAAGAAGGCTCAGG
TCTGGGATTCACTGTCAGGAGGGACAGATGTGGAGCAAAATCAATCACGGTCCACAGGGTGTGTTCTCA
GGGGGGGCTCTCAGGAAGGCAACTATGAAACCGAGGGGATTTCCTCTGTCAGTCACGGGCCCTCACTGGC
TGGCTTAGCCCACGGGAATGTCAGGTTCTGCAAGGCTGCCACAGCCTGCCACAAAGATGCCCTCGTGTCAI
CAAGAAAGGGATGATCAGCCACGGGCTCTGCCCGCAGGACCTCCACAGGAATGGGAAGGTTGCT
GTCCAGAAAGACCATCCCCCTGGAGGCTGGCATGGGAGAAGTGTGGCTGTACACGATGCTCTGTTGA
AGTGTGAAGACCTGGCTGGGACTGAGTCGGATGGGAAATCATCGGTGACGGGAGATGGGCC
CTTGGCTTAAAGAGTGTACAAAGGTGCTGGCTGGCTGAACAGCTGGAATAATAGAAGCTGGAGATGAAAT
10 TCTGCTTAAATGGGAACCTCTGCTGGCTCATGCACTTGTGCGCTGAATTATGAAGTCTGCCCC
AGAAGGACCTGTGCAAGTTAAATTAAAGAGCATAGGAATTCTCATGAATTAAACAAAGAATCATTTCTC
AGTTCCTCTCTTCACTGAAATCAGAGTCACTCTTAAACACAGGTGTTGAATGGCAACACTGGT

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In a search of public sequence databases, the NOV8a nucleic acid sequence, located on chromosome 5 has 997 of 1128 bases (88%) identical to a Papin mRNA from *Rattus norvegicus* (GENBANK-ID: AF169411). Public nucleotide databases include all GenBank databases and the GeneSeq patent database.

5 SNP data for NOV1a can be found below in Example 3.
The disclosed NOV8a polypeptide (SEQ ID NO:25) encoded by SEQ ID NO:24 has 2814 amino acid residues and is presented in Table 8B using the one-letter amino acid code. Signal P, Psort and/or Hydropathy results predict that NOV8a has no signal peptide and is likely to be localized in the nucleus with a certainty of 0.7000. In other embodiments, NOV8a may also be localized to the microbody (peroxisome) with a certainty of 0.3000, the mitochondrial matrix space with a certainty of 0.1000, or the lysosome (lumen) with a certainty of 0.1000.

Table 8B. Encoded NOV8a protein sequence (SEQ ID NO:25).

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MPTITQDNLVHLPLLYQWLQLNQLQEGGDGPQEQLCQAAIQKQLQEYIQLNFAVDESTVPPDHSPPEMEICTVY
LTKELGDTETVGLSGNIPVFQDYGEKRRGGKKRTHQGPVLDVGCIVWTELRKNSPAGKSGKVRLRDEILS
LNGQLMVGVDVSGASYLAEQCWNNGFIYLIMLRRFKKAHSTYNGNSNSSEPGETPTLELGDRTAKKGKRTR
RKFGVISRPPANKAPEESKGAGCEVSSDPSTELENGLDPELGNGHVFQLENGPDSLKEVAGPHLERSEVDR
GTEHRIPKTDAPLTSNDKRRFSKGKTFDQSSDCLARSKEEVRIWKMEELLKESDGLGIQVSGRGSKRS?P
HAIVVTVQVKEGGAHRLRDGRSLSLGDELLVINGHILLVGLSHEEAVAILRSATGMVQLVVASVKVGVLSAFQMP
GTDEPQDVCGAEESKGNLLESPKQGSNKIKLKSRLSGRWGLYLMQPVGGVHLLESVEEYNELMVRNGDPRIRM
LEVSRDGRKHSLPQLLDSSSASQEHIVKKSTRSLTTQVESPWRLIRPSVISIIGLYKEKGKGLGFSIAGG

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RDCIRGQMGIFVKTIFFNGSAEDGRLKEGDEILDVNGIPIKGLTFQEAHTFKQIRSGLFVLTVRTKLVSP
SLTPCSTPHMSRASPNTGGASAGGSDEGSSSLGRKTPGKDRIVMEVTLNKEPRVGLGIGACCLAL
ENSPPGIYIHSLAPGSVAKMESNLRSGSILEVNSVNRHAALSKVHAILSKCPGPVRLVIGRHNPKVNV
SEQEMDEVIASTYQESKEANSSPGLGTVISIGCFLLQDLSISETSQVFAHDVPGPLSDFMVAGSEDED
HPGSGCSTSEEGSLPPSTSTKEPGKPRANSVTLGSHRASGLFHQVTVAROASLPGSPQALRNPLLQRK
VGCYDANDASDEEFDRGDCISLPGALPGPIRPLSEDDPRRVSISSSKGMDVHNQEERPRKTLVSKAISAP
LLGSSVDSLLEESIPEGMVDAASYAANLTDSAEAPKGSPGSWWKKELSGSSSAPKLEYTVRTDTQSPINTGPS
SPQQKSEGLGSRHRPVARVSPHCKRSEAEAKPGSGTQVNLTGRANDPCLLDLSRVQATSVKTVAGFQPGGAV
EKESLGKLTGDACVTSCELASALSHLDASHLTENLPKAASELGQQPMTLEDSSSDLISSPGKKGAHPDP
SKTSVDIIGKVSRRPENESQPASPRVAKCKARSPVRLPHEGSPSPGEKAAAPPDYSKTRSASETSTPHNTRRVA
ALRGAGPDAEGMTPAGAVLPGDPLTSQEQRQGAPCGNHSKALEMTGIHAPESSQEPSPNLLLEGADSVSSRAPQAS
LSMLPSTDNTKEACGHVGHCPCGGSRSPVTDIDSFIKEDASAQSPSSQTGDGSQEGSAQGHPPAGAG
GGSSCRAEPVPVGGQTSPRRAWAAGAPAYPQWASQPSVLD SINDDKHFVNVNFKLSNYSRNFFSFHEDSTS
SGLGDESTPSLSSMYGDAEDSSSDPESLTEAPRASARDGWSPPRSRVLHKEDPSESEEQIEICSTRGCPN
PPSSPAHLPTQAAICPASAKVLSLKYSTPRESVASPREKVACLPGSYTSGPDSSQPSLLEMSSQEETHAD
ISTSNQHRSRSCAETTEVTASSAMENSPLSKVRHFTHSPPILSSPNMVNGLEHDLDDETLNLQYETSINA
AASLSSFSVDPKNGEVLENHISQESDQLLQPKMIARRPIMAWFKEINKHNQGTHLRSKTEKEQPLM
PARSPDKSIQMVSNSQQKGTVPHSPPPQPKTNLENKDLSKKSPAEMLLTNCQAKCGPKLKLRLSLKGAKVN
SEAPAANAVKAGGTDHRKPLISPQTSHTLSKAVSQRLLHVADHEDPDRNTTAAPRSQCVCLESKPPLATSGP
LKPSVSDTSIRTFSVPLTSPKPVPEQGMWSRFHMAVLSEPDRGCPPTPKSPKCRAEGRAPRADSGPSPAAS
RNGMSVAGNRQSEPRLAQHVAADTAQPRPTGEKGGNMMASDRLERTNQLKTVIESAEAVSETVCGNKPAESD
RRGGCLAQGNCQEKSIRLYRQVAEESTSHPSSLPSHASQAEQMSRSFSMAKLASSSSSLQTAIRKAEYSQ
GKSSLMSDRGVPRNSIPGGPSGEDHLYFTPRTPATRTYSMPAQFSSHFGREGHPPHSLGRSRDSQVPTSSV
VPEAKASRGGLPSLANGQGTVSVKPPLDTSRNLPATDEGDIISVQETSLCLVIDKIKVTRHYCYEQNWPHE
TSFFSVKQRIKFENLANADRPFVAKSGASPFLSVSSKKPPIGRSSSGSIVSGSLCHPGDAAARLLRRSLSSCS
ENQSEAGTLLPQMAKSPSIMLTISRQNPPETSSKGSDSELKKSLLGPLGIFTPTMTLSPVKRNKNSVRHTQ
PSPVSRSKLQELRALSMPDLDKLCSEDYSAGPSAFLKTELEITPRRSPGPPAGGVSCPEKGNNRACPGGSG
PKTSAAEPTSSASDTGEAAQDLPFRRSWSNLDDQLVSAQDQQRLQSVLSSVGSKSTILTLIQEAKAQSENE
EDVCFIVLNRKEGSCLGFSVAGGTDVEPKSITVHRVFSQGAASQEGTMNRGDFLLSVNGASLAGLAHGNVLU
VLHQALQHDKDALVVIKKGMDQPRPSARQEPPTANGKLLSRKTIPLEPGIGRSVAHDALCVELKTSAGLG
LSLDGGKSSVTGDGPLVIKRVYKGAAEQAGITIEAGDEILAINGKPLVGLMHDAWNIMKSVPEGPVQLLIR
KHRNSS

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A search of sequence databases reveals that the NOV8a amino acid sequence has 937 of 1741 amino acid residues (53%) identical to, and 1133 of 1741 amino acid residues (65%) similar to, the 2766 amino acid residue Papin protein from *Rattus norvegicus* (Q9QZR8) (E = 5 0.0), and 122 of 304 amino acid residues (40%) identical to, and 176 of 304 amino acid residues (57%) similar to, the 334 amino acid residue Human interleukin-16 monomer (patp:AAW19209) (E = 1.0e⁻⁴⁶). Amino acid databases include the GenBank databases, SwissProt, PDB, PATP, and PIR. The global sequence homology (as defined by FASTA alignment with the full length sequence of this protein) is 72.943% amino acid homology and 10 69.689 % amino acid identity. In addition, this protein contains the following protein domains (as defined by Interpro) at the indicated nucleotide positions: *PDZ domains* (IPR001478) at amino acid positions 336 to 422, 558 to 644, 700 to 784, 2597 to 2681, 2725 to 2810.

15 NOV8a is expressed in at least the following tissues: Nervous System. Brain. Prosencephalon/Forebrain. Diencephalon. Pituitary Gland; Hematopoietic and Lymphatic System. Hematopoietic Tissues. Lymphoid tissue. Lymph node; Whole Organism. In addition, the sequence is predicted to be expressed in the following tissues because of the expression pattern of (GENBANK-ID: AF169411) a closely related Papin homolog in species *Rattus norvegicus*: brain. TaqMan data for NOV8 can be found below in Example 2.

NOV8b

A disclosed NOV8b nucleic acid of 8640 nucleotides (also referred to as CG57026-04) encoding a novel papin-like protein is shown in Table 8C. An open reading frame was identified beginning with an ATG initiation codon at nucleotides 101-103 and ending with a TGA codon at nucleotides 8534-8536. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 8C. The start and stop codons are in bold letters.

Table 8C. NOV8b nucleotide sequence (SEQ ID NO:26).

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AGCTGATGATGGCCAGGGACCCCAGGGACGTGGGGCCCTGTGGGGTCTGGCCCCCAGGAGCAAGACCTCTG
ATGATGCTGGTGTCTGGGAGTGACCCATGCCCATACCCAGGAATGCCGTCTGCACCTGCCCTCT
CTACCAGTGGCTGCAGAACAGCCCTGAGGAAGGTGGGGATGGGCCGAGCAGGGCTCTGCCAGGCCAT
CCAGAAGCTGCCAGGAGTACATCCAGCTGAACCTTGCTGTGGATGAGAGTACGGTCCCACCTGATCACAGCC
CCCCGAAATCGGAGATCTGACTGTGACCTCAGGAAGGAGCTGGGGGACACAGAGACTGTGGGCTGAGTTT
TGGGAAACATCCCGTGTGGGACTATGGTAAAAGCGCAGGGGGGAGAAGAGGAAAACCACAGGG
TCCGTGCTGGATGTGGGCTGCATCTGGGTGACAGAGCTGAGGAAGAACAGCCAGCAGGAAGAGTGGAA
GGTCGACTCGGGATGAGATCTCTCACTGAATGGCAGCTGATGGTTGGAGTGTGACTGAGCTGGGGCCAG
TTACCTGGCTGAGCAGTGTGGAATGGCGCTTATCTACCTGATCATGCTGCCGCTTTAACACAAGC
CCACTCCAATTATAATGCCAACACTAGCAACAGCTGAAACCCAGGAGAACACCTAACCTGGAGCTGGGTGA
CCGAACTCGGAAAGGGGAAACGAGAACAGGAAAGTGGGGTCACTCCAGGCCCTCTGCCAACAAAGGCCCC
TGAAGAACATCCAGGGCAGCTGGCTGTGAGGTCTCAGTGACCCAGCACTGAAGCTGGAGAACGGCCCTGGA
CCTGAACTGGAAACGCCATGCTTCACTGAGAACATGGCCAGATTCTCTCAAGGAGGTGGCTGAGC
CCATCTAGAGAGGTCAAGAGTGGCACAGGGACAGACATAGAACATTCAAAGACAGATGCTCCCTGACCAC
AAGCAATGACAACAGCCCTCTCAAAGGTGGGAACAGGACTCTCAATCGAGTGAATGCCCTGGCACGGTC
CAAGGAGGAGTGGGGCAATATGGAGATGGAGCTGCTCAAAGAACATGGATGGCTGGGAATTAGTTAG
TGGAGGCCAGGATCAAAGCCTCACCGCTACGCTATGCTACTCAAGCTGAAGGAAGGGAGTGGCTCA
CAGGCTCAGGGATGGCAGGCTGCTTAGAGATGAGCTGCTGGTAACTCAATGGTCACTTACTGGCTGGGCT
CTCCCACGAGGAAGCAGTGGCATTCTCGCTCCGCCACGGGAATGGTGAGCTGTGGTGGCAGCAAGGT
AGGTGTGTTCTGCATTCAGATGCCCTGGGACAGATGAACCCCAAGATGTGCTGGTGTGAGGAATCAA
GGCGGAACTTCCAAAGTCCAAACAGGGCAACAAATTAACAGCTCAAGGACTGGCCTTTCAGGTAGGTGGGG
GCTTACCTGATGCCAGCTGTGGGGGTGACACCCCTTGTGAGCTGTTGAGAACATAACAGGCTGATGGT
GCCGAATGGGACCCCCGATCCGGATGTTGGAGGTCTCCGGAGATGGCCAGAACACTCCCCCGCAGCT
CTGGACTCTTCCAGTCCCTCACAGGAATACCAATTGTGAAGAAGTCTACCCCTCTTAAGCACGACTCA
GGTGAATCTCTCGGGAGGCTATTCCGCCATCCGTATCTCGATATTGGTTGTACAAAGAAAAGSCAA
GGGCTTGGCTTAGTATGGCTGGAGGAGCTGGAGACTAAAGAGGGATGAAATCTAGATGTAATGGAAAT
CTTCCCAAATGGATCAGCTGCAGAGGAGACTAAAGAGGGATGAAATCTAGATGTAATGGAAAT
ACCAATAAGGGCTTGACATTCAAGAAGCATTCACTTTAACAAATCCGAGTGGATTATTGTTT
AACGGTACCCACAAGTGGTGAACCTCAACCCCTGCTGCCACACCCACACATGAGCAGATCCG
CTCCCCGAACCTCAATACCAAGTGGGGAGGCCCTCGCGGGAGGTTCCGATGAAGGAGTTCTCATCCCTGG
TCGGAAAGACCCCTGGGCCAAGGACAGGATGCTATGGAGTAACACTCAACAAAGGCAAGAGTGGGATT
AGGCATTGGCTGCTGTGGCTGGGACAGGATGCTTACGGGATCTACATTCAAGGCTTGCTCCAGG
ATCAGTGGCAAGATGGAGAGCACCTGAGCCGGGATCAATCTGGAGTGAACCTCCCTCAAGTCCG
CCATGCTGCTTAAGCAAAGTCCACGCCATCTTGAATTGGCTCCAGGACGGTTGCCCTGTGATCGG
CCGGCACCTAACTCAAAGGTTCCGAGCAGGAATGGATGAAGTCAAGCACGCCAGCACTTACAGGAGAG
CAAAGAGGCCATTCCCTCTGGCTAGTACCCCTTGAGAGACTCCCTCTCTGCAAAAAGGACTCCCT
TATTCTGAATCTGAACCTCCAGTACCTTGCCCACTGGCTGGCCCTTGCTCAGACTTACGGTGGGT
CGGTTCTGAGGAGCAGGAGTACCCGGGAAGTGGCTGAGCAGCTGGAGGAGGGCAGGCTGCCCTCCACAC
CTCCACTCAAGGGAGCTGGAAAACCCAGGCCAACAGCCCTGTAACCTTGGAGCCATGGGCTTCTGG
GCTTCCACAAGCAGGTGACAGTGGCTGAGACAAGGAGCTCTCCCGGAAGGCCACAGGCCCTCCGAAACCC
TCTCCCTCCGAGAGGAAGGTAGGCTGCTACGATGCCAACGATGCCAGTGAAGGAGAGTTGACAGAGA
AGGGGACTCCATTCACTCCCAAGGGGCCCTCCGGTCCCATCAGGCCCTGTGAGAGGATGACCCGAGGCG
TGTCTCAATTCTCTTCCAAAGGGCATGGACGCTCAACAGGCCAACAGCCCTGTAACCTTGGAG
CAAGGCCATCTGGCACCTCTTGTGAGCTGAGCTTGGACTTGGAGAGTATCCAGAGGGCATGGTGG
TGCTGCGTCTATGCCACCAACCTCACGGACTCTGAGAGGCCCTGGAGGGAGCCCTGGAAGCTGGTGGAA
GAAGGAACGTGAGGATCAAGTAGGCACCCAAATTGGAATACACAGTCCGTAAGACACCCAGAGTCCGAC
AAACACTGGGAGCCCGAGTCCCTGGGAGGGCTGGCTCACAGACAGGAGTCCAGGCCACAGGCCAGTGGCCAG
GGTAAGCCCCACTGCAAGAGATCCGAGGCTGAGGCCAAGGGCAGTGGCTCACAGACAGTGAACCTGACTGG
CAGGCCAATGATCCATGCCATCTGGAATCTGAGAGTCCAGGCCACTTGTCAAAGTGAATGACTGCTGCTGGCTT

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TCAGGCCAGGTGGAGCTGTGAGAAGGAATCTCTGGAAAGCTGACCACTGGAGATGCTTGTGCTTACCCAG
 CTGTGAACTAGCCAGTGCTCTGTCCCACCTGGATGCCAGGCCACCTCACAGAGAACCTGCCAAAGCTGCATC
 AGACCTGGGCAACAAACCCATGACTGAACCTGGACAGCTCTCGGACCTCATCTCTTCCCCAGGGAAAGAAGGG
 GCGCGCTCATCTGACCCCAGCAAGACCTCTGTAGAACACAGGGAAAGTCAGTGGCCAGAGAACATCCCAGCCA
 GCCTCATCGCCAGGGTCCCAGTCAAGGCAAGGTCTCCAGTCAGGCTCCCCATGAGGGCAAGCCCCCTC
 CCCAGGGAGAAAGCAGCGCTCCCCCTGACTCACAGCAAGACTCGATCAGCATCGAACACCAGCACACCCCA
 CAATACAGGAGGGTGGCTGCCCTCAGGGAGCGAGAACAGGGAGCTCAGGTAACACAGTAAGGCTCTGGA
 CCTGCAAGGAGACCCCTCACATCAGGAGCGAGAACAGGGAGCTCAGGTAACACAGTAAGGCTCTGGA
 AATGACAGGAATCCATCACCTGAAAGCTTCCCAGGAGCTCCCTGTGGAGGGAGCAGATTCTGTGCTCTC
 AAAGGCCAGGCCAGGGCAACCTCTTCACTGCTCATGACAAACACCAAAAGAAGCATGTGGCATGTCTC
 GGGCACTGCTGCCGGGGGAGTAGAGAGAGCCCTGTGACGGACATTGACAGCTTCATCAAGGAGCTGGA
 TGCTTCTGAGCAAGGTCTCCGCTCTCCAGACGGGGAGCTGGCTCTCAGGAGGGCAGTGTCTAGGGCCA
 CCCACCAAGCCGGGGCTGGAGGTGGGAGCTCCCTGCGCTGCCAACAGTCCCAGGGGGGAGAACCTCTCCCC
 GAGGAGGGCCTGGCTCTGTGCTGGCCCTAACATGGGCTCCAGGGCTTCTGGTTTAGATTCAAT
 TAATCCCAGAACAAACATTACTGTGAAACAAAAACTTCTGAGCAACTACTCTAGAACATTTTAGCAGTTTCA
 TGAAGACAGCAACCTCCATCAGGCCCTGGGTGACAGCACGGCCCTGTGACATCCATGTAAGGCGATGC
 TGAGGATTCTCTCTGACCCCTGAGTCAGTCAGCAAGGCCCACAGGCTTCTGCCAGGGAGCGCTGGTCCCC
 TCCCTGTTCCCGTGTGTTGACAAGGAAGTCCTCGAGTCAGAAGAGGAACAGATTGAGATTGTT
 CACAGCTGGCTGCCCAATCACCCCTCGAGTCCTGCTATCTTCCACCCAGGGCTGCCATCTGTCTGCCCC
 AGCAGGAAAGTTCTGCTATAAAACATGAGCAACTCCAGGAGAGCTGGCTCTGGAGAACCTGGCTCTG
 TTGCCCAGGCTCATACACTCAGGCCAGACTCTTCCAGGACATCATCAGCTTGGAGATGAGCTCTCAGGA
 GCATGAAACTCATGCGGACATAAGCAGCTCACAGAACACAGGCCCTGTGAGAACAGGAAACACAGAAGT
 CACCAAGGCTAGCTCAGGAAACAGTCCGCTGCTAAAGTAGCCAGGCATTTCACAGTCCGCCCC
 CATTCTCAGCTCCCCAACATGGTAAATGGCTTGGAACATGACCTGAGATGACGAAACCCGAATCAATA
 CGAACAAAGCATTAATGAGCTGCCAGTGTGCTCTGGATGTGCTTAAAGAACATGGAGAACATCTGT
 TTGAAAACCTCCACATCTGAGGAAAGCTAACGACTCTGGATGACTCTGCTACAGAACAAAAATGATCGCTAG
 GAGGCCCATCATGGCTCTTTAAAGAAATAAAACATAACCAAGGCAACACATTGGAGGAGAACACCGA
 GAAGGAACACCTCTAATGCGTGGAGACTCCGACTCCAAGGAAAGTCAGATGGTGGATTCAAGCCAAAAAA
 GGGCGTTACTGTGCTCATAGCCCTCTAGCCGAAACACCTGGAAAATAAGGACCTGCTAAGAAGAG
 TCCCGCAGAAATGCTCTGACTAATGCTGAGAACGCAAAGTGTGCTTGGAGGCTAGCCTCAA
 GGGCAAGGCCAAAGTCACACTCTGAGGCCCTCTGCGAATGCTGAGGAGGGCAGGGGAGCGGACCAAGGAA
 ACCCTGTATCTACCCCAAGCTCCACAAAACACTCTAAGGCACTGTGCTACAGGCCCTCCATGAGCCGA
 CCAAGGAGGCCCTGAGAACACACCCAGCTGCCCTCAGGTTCCCTGTGCTGGAAAGCAAGGCCACC
 TCTGCCACCTCTGGGCACTGAAACCCCTCAGTGTGCTGACACGAGCATCAGGACATTGTCTGCCCTGAC
 CTCTCCCAAGCTGTCTCTGAGCAAGGCATGTGAGGCAGGTTCCACATGGCTGTCTCTGTAACCCGACAG
 AGGTTGCCAACCCCTAAATCTCTAAAGCTGAGGAGGGCAGGGCTGGGGAGCGGACCAAGGAA
 ACCCTGTATCTACCCCAAGCTCCACAAAACACTCTAAGGCACTGTGCTCTCTCCCTCTTCAAACAGCCATTAG
 AAAGGCAAGAAACTCCAGGGAAATAAGGCTGATGTAGACTCTCCAGGGGTGCCAGAACAGCATTCC
 AGGGGCCCTCGGGGAGGACCATCTACTTCACCCCAAGGCCAGGACCCAGACTCTCATGCCAGC
 CCAGTTCTCAAGCCATTGGACGGGAGGGTCACCCCTCACAGGCCTGGCTCTCTGGGACAGCCAGGT
 CCTCTGAGAACAGCTGTTGCTCCGGAGGCAAGGCATCAGGAGGTGCTTCCAGGCCATGGCTAATGGACA
 GGGCATATATGTAAGGGCTGCTGGACACATGGAGAACATCTCCAGGAAACAGATGAGGGGATATCAT
 TTCAGTCAGGAGACAGGCTGCTAGTCAGACAAAGTCAACAGAACACTACTGCTATGAGCA
 GAACAGGCCATGAACTCTACCTATTCTGAGAACAGGCCATCAAGTCTTTTGTGAGAACCTGGCAA
 TGCTGACCGGCTGTAGCCAAGTCGGGGCTTCCCATTGGCTGGTGAGCTTCAAGGCCCTCCATTGGAG
 CGGGCTTCTGGCAGCATTTGTTCTGGAGCTGGCCACCCAGGTGACGGAGCAAGGTTGGAGACG
 CAGCTTGTGAGTTCTGAGCGAACAAAGGCAAGGCCACCTGGCTCTCTGGCCATGGCTTCTCC
 AATCATGACACTGACCATCTCTGGCAGAACCCACAGAGAACAGCTGAGCAAGGGCTGTGATTGGAACTAA
 GAAATCACTTGGCTTGGAAATTCCCACCCCAAGATGACCTGGCTTCTCTTCAAGAGAACACTC
 CTCGGTACGCCACAGCAGCCCTGCCGTGCTCCCTCAGCTCCAGGAGCTGAGAGGCCCTTGAGCATGCC
 TGACCTTGACAAGCTCTGAGCGAGGATTACTCAGCAGGGCCAGGCCGTGCTCTTCAAAACTGAGCTGGA
 CATCACCCCCAGGGAGCTACCTGGGCTCTGTGAGGGCTTCTGGCTGGCCAGATGGCCAAGTCTCC
 CTGTCAGGGAGGAGCTGGCCCTAAACAGTGTGCTGAGAACCCAGTCTGGCTGGAGCTGAGTACGGGT
 TGCCAGGAGATCTGGCTTGGAGAACAGCTGGTCAAGTAAATTGGATCAACTCTAGTCTCAGGGGGG
 GCAAAAGATTACAGTGTGTTTATGTCAGTGGGATCGAAATCTACCATCTAACCTCTCATTCAGGAAGG
 AGCACAATCAGAGAACATGAGAACAGATGTTGCTTCACTAGTCTGAAATGAAAAGAAGGCTCAGGCT
 CAGTGTGGCAGGAGGGACAGATGTGAGGAAATCAACAGCTGCTCCACAGGGTGTGTTCTCAGGGGG
 TTCTCAGGGAGGGACTATGAAACCGAGGGGATTTCCTCTGTGAGTCAGTCAACAGGCCCTCAGTGG
 CCACAGGGAAATGTCCTGAGGTTCTGCAACAGCACAGCTGCAAAAGATGCCCTGTGGTCA
 GATGGAGTACGGCCAGGGCTCTGCCGGAGGCTCCACAGGCAATGGGAAGGGTTTGCTGCTCAGAAA
 GACCATCCCCCTGGAGGCTGGCATTGGAGAACAGTGTGGCTGACAGATGCTCTGTGTTGAGTGCTGAA
 GACCTCGCTGGGCTGGGACTGACTGCTGGATGGGAAATCATCGGTGACGGAGATGGGCCCTGGT
 TAAAGAGTGTACAAAGGTGGCTGGCTGAACAGCTGGAATAAGAAGCTGGAGATGAAATTCTGCTAT
 TAATGGGAAACCTCTGGCTTGGCTCATGCACTTGTGATGCCCTGGAAATTATGAGACTCTGCT
 CAGGGACC

TGTGCAGTTATTAAATTAGAAAAGCATAGGAATTCTTCATGAATTAAACAAGAACATTTCTCAGTTCTCTT
CTTCTTAGCAAATCAGAGTGACTCTTAAACCAACAGGTGTTGAAATGGCCAACACTGGTACAGACACG

In a search of public sequence databases, the NOV8a nucleic acid sequence, located on chromosome 5 has 5828 of 5941 bases (98%) identical to a gb:GENBANK-ID:AF338650|acc:AF338650.1 mRNA from *Homo sapiens* (*Homo sapiens* PDZ domain-containing protein AIPC (AIPC) mRNA, complete cds) (E = 0.0). Public nucleotide databases include all GenBank databases and the GeneSeq patent database.

The disclosed NOV8b polypeptide (SEQ ID NO:27) encoded by SEQ ID NO:26 has 2811 amino acid residues and is presented in Table 8D using the one-letter amino acid code. Signal P, Psort and/or Hydropathy results predict that NOV8b has no signal peptide and is likely to be localized in the nucleus with a certainty of 0.7000. In other embodiments, NOV8b is also likely to be localized to the microbody (peroxisome) with a certainty of 0.3000, the mitochondrial matrix space with a certainty of 0.1000, and to the lysosome (lumen) with a certainty of 0.1000.

Table 8D. Encoded NOV8b protein sequence (SEQ ID NO:27).

MPITQDNAVLHLPLLYQWLQNSLQEGGDGPEQRQCQAAIQKLQEYIQLNFAVDESTVPPDHSPPEMEICTVY
LTKELGDTETVGLSFGNIPVFGDYGEKRRGGKKRTHQGPVLDVGCIWVTELRKNSPAGKSGVRLRDEILS
LNGQLMVGVDFVGASYLAEQCWNGGFYIYLMLRRFKHKASTYNGNSSNSEPGETPTLELGRTAKKGRT
RKFGVISRPPANKAPEESKGSAGCEVSSDPSTELENGLDPELGNHVFQLENGPDSLKEVAGHLERSEVDR
GTEHRIPKTDAPLITSNDKRRFSKGKTDQFQSSDCLARSKEEVGRIWKMELLKESDGLGIQVSGGRGSKRSP
HAIVVTQVKEGGAHARLRDGRSLGDELLVINGHLLVGLSHEEAVALRSATGMVQLVVASKGVLSAFQMP
GTDEPQDVCGAAEESKGNLIESPKQGSNKIKLKSRLSGRWGLYLMQPVGVVRLESVEEYNELMVRNGDPRIRM
LEVSRDGRKHSLPQLLSDSSASQEHYIVKNGKSTRSLTTQVESPRLIRPVSVISIIGLYKEKGKGLGPSIAGG
RDCIRGQMGIFVKTIFPNSRASDGGTQVQKQFQTAHFTKQIRSGLFVLTIVRTKLVSP
SLTPCSTPTMSRSASPNTSGASAGGSDEGSSSLGRKTPGPKDRIVMETLNKEPRVGLGIGACCIAL
ENSPPGIYIHSIAPGSTVAKMESNLRSRGDQILEVNSVNVRHAALKSVHAILSKCPPGVRLVIGRHPNPKVSE
QEMDEVILARSTYQESKEANSSPGLGTPLKSPSLIAKDDSLIISESELQSYFAHDVPGPLSDFMVVGSEDEDHPG
SGCSTSEGSLLPPSTSTKEPGKPRANSLVTLGSHRASGLFHQVTVQASLPGSPQALRNPLLQRKVGC
YDANDASDDEEEFDREGDCISLPGALGPPIRPLSEDPPRVSISSSKGMDVHNQEEPRKTLVSAIASAPLLG
SSVDELEESIPEGMDVAASYAANLTDSEAAPKGSPGSWWKKELSGSSAPKLEYTVRDTDQSPTNTGSPSSPQ
QKSEBLGSRHRPVARVSPHCKRSEAEAKPGSQTVNLTRGRANDPCDLDLSRVQATSVKVTVAGFQPGGAVEKE
SLGKLTGDCAVSTSCELASALSHLDASHLTENLPKAASELQGQQPMTELDSSSDLISSPGKKAAHPDPSKT
SVDTGKVSRPENPSQASPRVAKCARSVPVRHGPSPGSEKAAPPDYSKTRSETSTPHNTRRVAALR
GAGPGAEGMTPAGAVLPGDPLTSQEQRQGAPGNHSKALEMTGIHAPESSQEPSSLEGADSVSSRAPQASLSM
LPSTDNTKEAGHVSGBHCPGGSRESPVTIDDSFIKEELDASAARSPSSQTGDSQEGSAQGEPAGAGGGS
SCRAEPVPGQTSSPRRAWAAGAPAYPOWASQPSVLDWINPDKHTVWNKNFLNSYRNFSSFHEDSTSLSGL
GDSTEPSLSSMYGDAEDSSSDPESLTEAPRASARDGWSPRSRVSLSHKEPDPSSEEEQIEICSTRGCPNPPS
SPAHLPTQAICPASAKVLSKYSTRESVASPREKVACLPGSYTSGPDSQSSQPSLLEMSSQEHETHADIST
SQNHRPSCAETTEVTSASSAMENSELSKVARHHSPPILSSPNMVNGLEHDLLDDETINQYETSINAAS
LSSFSVDPKNGESVLENHISSESDQLDQQPKMIIARRPMIAWKEINKHNQGTHLRSKTKTEQPLMPAR
SPDKSIQMVSQSSQKKGVTVPHSPPKPTNLENKDLSSKSPAEMLLNTNGQKAKCGPKLKRLSLKGAKVNSEA
PAANAVKAGGTDRKPLIISPQTSKHTLSKAVSQRHLVADHEDPDRNTTAAPRS PQCVLESKPPLATSGPLKP
SVSDTSIRTFSPLTSKPKVPEQGMWSRFHMAVLSEPDRGCPTTPKSPKCRAGEPRADSGFVSPAASRNG
MSVAGNRQSEPRLAGHVAADTAQPRETGEGKGNIMASDRLERTNQLKIVEISAEVSETVCGNKPAAESDRRG
GCLAQGNCQEKESEIRLYRQVAEESSTSHPSSLPSHASQAEQEMSRSFSMAKLIASSSSLQTAIRKAEYSQGKS
S1MSDSRGVPRNSIPGGPSEGDEHDLYFTPRPATRTYSMPAQFSSHFREGHPPHSLGRSRDSQVFTSSVVE
AKASRGGLPSLANGQGIYSVKPLLDTSRNLPATDEGDIISVQETSCLVTDKIKVTRRHCYEQNWPHESTSF
FSVKQRIKSFENLANADRPVAKSGASPLSVSSKPPIGRRSSGSIIVSGSLGHPGDAAARLLRRSLSSCSENQ
SEAGTLLPQMAKSPSIMLTISRQNPPETSSKGSDSELKKSLGPLGIPTPTMTLASPVKRNKSSVRHTQSP
VSRSKLQELRALSMPPDLDKLCSEDYSAGPSAVLFKTEBLEITPRRSPGPAGGVSCPEKGNNRACPGGSGPKT

SAAETPSASDTGEAAQDLPFRRSWSVNLDQQLVSAGDQQRLQSVLSSVGSKSTILTLLQEAKAQSENEDV CFIVLNRKEGSCLGFSVAGGTDEVPKSITVHRVFSQGAASQEGTMNRGDFLLSVNGASLAGLAHGNVLKVHL QAQLHKDALVVIKKGMQPRPSARQEPPTANGKGLLSRKTIPLPEPGIGRSVAVIDALCVEVLKTSAGLGLSL GGKSSVTGDGPLVIKRKYKGAAEQAIIAEAGDEELAINGKPLVGLMHFDAWNIMKSVPEGPVQLLIRKHR NSS

A search of sequence databases reveals that the NOV8a amino acid sequence has 2017 of 2045 amino acid residues (98%) identical to, and 2022 of 2045 amino acid residues (98%) similar to, the 2641 amino acid residue ptnr:TREMBLNEW-ACC:AAK07661 protein from 5 *Homo sapiens* (Human) (PDZ DOMAIN-CONTAINING PROTEIN AIPC) (E = 0.0). Public amino acid databases include the GenBank databases, SwissProt, PDB and PIR.

NOV8b is expressed in at least the following tissues: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, 10 lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea and uterus. Expression information was derived from the tissue sources of the sequences that were included in the derivation of the sequence of CuraGen Acc. No. CG57026-04. The sequence is predicted to be expressed in the following tissues because of the expression pattern of 15 (GENBANK-ID: gb:GENBANK-ID:AF338650|acc:AF338650.1) a closely related *Homo sapiens* PDZ domain-containing protein AIPC (AIPC) mRNA, complete cds homolog in species *Homo sapiens* : prostate. TaqMan data for NOV8b can be found below in Example 2.

The NOV8a, and 8b proteins are very closely homologous as shown in the 20 alignment in Table 8E.

Table 8E Alignment of NOV8a, and 8b.

	10	20	30	40	50	60
25 NOV8a
	MPI	TQDN	AVLHLP	LLYQWLQNSL	QEGGDGPEQRLCQAAI	QKLQ
NOV8b	MPI	TQDN	AVLHLP	LLYQWLQNSL	QEGGDGPEQRLCQAAI	QKLQ
	Y	I	T	C	K	E
	70	80	90	100	110	120
30 NOV8a
	HSP	PMEI	CTVYLTKELGD	TETVGLSFGNIPVFGDY	GEKRRGGK	KRKT
NOV8b	HSP	PMEI	CTVYLTKELGD	TETVGLSFGNIPVFGDY	GEKRRGGK	KRKT
	Y	I	T	C	K	E
	130	140	150	160	170	180
35 NOV8a
	VTEL	RKN	SPAGKSGKVR	LRLDEILS	LNGQLMVGVDV	SGASYLAEQCWNGGFIY
NOV8b	VTEL	RKN	SPAGKSGKVR	LRLDEILS	LNGQLMVGVDV	SGASYLAEQCWNGGFIY
	Y	I	T	C	K	E
	190	200	210	220	230	240
40 NOV8a
	HKA	HSTYNGN	SSNSSEPG	ETPTLELGDR	TAKKGKRTRKF	GVISRP
NOV8b	HKA	HSTYNGN	SSNSSEPG	ETPTLELGDR	TAKKGKRTRKF	GVISRP
	Y	I	C	T	K	E

	250	260	270	280	290	300
NOV8a	EVSSDPSTELENGLDPELGNGHVFQLENGPDSLKEVAGPHLERSEVDRGTEHRIPKTDAP					
NOV8b	EVSSDPSTELENGLDPELGNGHVFQLENGPDSLKEVAGPHLERSEVDRGTEHRIPKTDAP					
5						
	310	320	330	340	350	360
NOV8a	LTTSNDKRFSKGKTDQFQSSDCLARSKEEVGRIWKMEPLLKESDGLGIQVSGGRGSKRSP					
NOV8b	LTTSNDKRFSKGKTDQFQSSDCLARSKEEVGRIWKMEPLLKESDGLGIQVSGGRGSKRSP					
10						
	370	380	390	400	410	420
NOV8a	HAIIVVTQVKEGGAHRLRDGRLSILGDELLVINGHLLVGLSHEEAVAILRSATGMVQLVVA					
NOV8b	HAIIVVTQVKEGGAHRLRDGRLSILGDELLVINGHLLVGLSHEEAVAILRSATGMVQLVVA					
15						
	430	440	450	460	470	480
NOV8a	SKVGVLASFQMPGTDEPQDVCGAEESKGNGLQESPKQGSNKIKLKSRSLSGRWGLYLMQPVG					
NOV8b	SKVGVLASFQMPGTDEPQDVCGAEESKGNGLQESPKQGSNKIKLKSRSLSGRWGLYLMQPVG					
20						
	490	500	510	520	530	540
NOV8a	VHRLESVEEYNELMVRNGDPRIMLLEVSRDGRKHSLPQLLDSSASQEYHIVKKSTRSLS					
NOV8b	VHRLESVEEYNELMVRNGDPRIMLLEVSRDGRKHSLPQLLDSSASQEYHIVKKSTRSLS					
25						
	550	560	570	580	590	600
NOV8a	TTQVESPERLIRPSVISIIGLYKEKGKGLGFSTIAGGRDCIRGOMGIFVKTIIFPNQSAED					
NOV8b	TTQVESPERLIRPSVISIIGLYKEKGKGLGFSTIAGGRDCIRGOMGIFVKTIIFPNQSAED					
30						
	610	620	630	640	650	660
NOV8a	GRLKEGDEILDVNGIPIKGLTFQEAIHTFKQIRSGLFVLTVRTKLVSPSLTPCSTPTHMS					
NOV8b	GRLKEGDEILDVNGIPIKGLTFQEAIHTFKQIRSGLFVLTVRTKLVSPSLTPCSTPTHMS					
35						
	670	680	690	700	710	720
NOV8a	RSASPNTSGASAGGSDEGSSSSLGRKTPGPKDRIVMEVTLNKEPRVGLGIGACCLAL					
NOV8b	RSASPNTSGASAGGSDEGSSSSLGRKTPGPKDRIVMEVTLNKEPRVGLGIGACCLAL					
40						
	730	740	750	760	770	780
NOV8a	ENSPPGIYIHSLAPGSVAKMESNLSRGS-ILEVNSVNVRHAALSKVHAILSKCPPGPVRL					
NOV8b	ENSPPGIYIHSLAPGSVAKMESNLSRGDILEVNSVNVRHAALSKVHAILSKCPPGPVRL					
45						
	790	800	810	820	830	840
NOV8a	VIGRHPNPKVNVSEQUEMDEViarstyQEsKEANSSPGLTVISIGCFLOODSLISESE					
NOV8b	VIGRHPNP--QVSEQUEMDEViarstyQEsKEANSSPGLTVIKS-PSCAKKDSLISESE					
50						
	850	860	870	880	890	900
NOV8a	LSQYFAHDVPGPLSDFMVAGSEDEDHPGSGCSTSEEGLPPSTSTKEPGKPRANSLVTL					
NOV8b	LSQYFAHDVPGPLSDFMVAGSEDEDHPGSGCSTSEEGLPPSTSTKEPGKPRANSLVTL					
55						
	910	920	930	940	950	960
NOV8a	GSHRASGLFHKOVTVARQASLPGSPQALRNPLLQRKVGCYDANDASDEEEFDREGDCIS					
NOV8b	GSHRASGLFHKOVTVARQASLPGSPQALRNPLLQRKVGCYDANDASDEEEFDREGDCIS					
60						
	970	980	990	1000	1010	1020
NOV8a	LPGALPGPIRPLSEDDPRRVSISSSKGMDVHNQEERPRKTLVSKAISAPLLGSSVDEES					
NOV8b	LPGALPGPIRPLSEDDPRRVSISSSKGMDVHNQEERPRKTLVSKAISAPLLGSSVDEES					
65						
	1030	1040	1050	1060	1070	1080
NOV8a	IPEGMVDAASYAANLTDSEAAPKGSPGSWWKKELSGSSSSAPKLEYTVRDTOSPTNTGSP					
NOV8b	IPEGMVDAASYAANLTDSEAAPKGSPGSWWKKELSGSSSSAPKLEYTVRDTOSPTNTGSP					
70						

	1090	1100	1110	1120	1130	1140	
5	NOV8a	SSPQQKSEGLGSRHPVARVSPHCKRSEAEAKPGSQTVNLGRANDPCDLSRVQATSV					
	NOV8b	SSPQQKSEGLGSRHPVARVSPHCKRSEAEAKPGSQTVNLGRANDPCDLSRVQATSV					
		1150	1160	1170	1180	1190	1200
10	NOV8a	KVTVAGFQPQGGAVEKESLGKLTGDACVSTSCELASALSHLDASHLTENLPKAASELGQQ					
	NOV8b	KVTVAGFQPQGGAVEKESLGKLTGDACVSTSCELASALSHLDASHLTENLPKAASELGQQ					
		1210	1220	1230	1240	1250	1260
15	NOV8a	PMTELDSSDLISSLPGKKAAHPDPSKTSVDTGKVSRRPENPSQAPRVAKCKARSPVRL					
	NOV8b	PMTELDSSDLISSLPGKKAAHPDPSKTSVDTGKVSRRPENPSQAPRVAKCKARSPVRL					
		1270	1280	1290	1300	1310	1320
20	NOV8a	PHEGSPSPGEKAAPPDYSKTRSASETSTPHNTRRAVALRGAGPGAEGMTPAGAVLPGDP					
	NOV8b	PHEGSPSPGEKAAPPDYSKTRSASETSTPHNTRRAVALRGAGPGAEGMTPAGAVLPGDP					
		1330	1340	1350	1360	1370	1380
25	NOV8a	LTSQEQRQGAPGNHSKALEMTGIGHAPESSQEPSSLLEGADSVSSRAPQASLSMLPSTDNTK					
	NOV8b	LTSQEQRQGAPGNHSKALEMTGIGHAPESSQEPSSLLEGADSVSSRAPQASLSMLPSTDNTK					
		1390	1400	1410	1420	1430	1440
30	NOV8a	EACGHVSGHCCPGGSRESPVTIDSFIFKELDDASAARSPSSQTGDSGSQEGSAQGHPPAGA					
	NOV8b	EACGHVSGHCCPGGSRESPVTIDSFIFKELDDASAARSPSSQTGDSGSQEGSAQGHPPAGA					
		1450	1460	1470	1480	1490	1500
35	NOV8a	GGGSSCRAEPVPFGQTSSPRRAWAAGAPAYPQWASQPSVLDSINPDKHFTVNKNFLSNYS					
	NOV8b	GGGSSCRAEPVPFGQTSSPRRAWAAGAPAYPQWASQPSVLDSINPDKHFTVNKNFLSNYS					
		1510	1520	1530	1540	1550	1560
40	NOV8a	RNFSSFHEDSTSLSGLGDSTEPSPSLSSMYGDAEDSSSDPESLTERAPRASARDGWSPPRS					
	NOV8b	RNFSSFHEDSTSLSGLGDSTEPSPSLSSMYGDAEDSSSDPESLTERAPRASARDGWSPPRS					
		1570	1580	1590	1600	1610	1620
45	NOV8a	SLHKEDPSEEEEQIEICSTRGCPNPSSPAHLPTQAAICPASAKVLSLKYSTPRESVAS					
	NOV8b	SLHKEDPSEEEEQIEICSTRGCPNPSSPAHLPTQAAICPASAKVLSLKYSTPRESVAS					
		1630	1640	1650	1660	1670	1680
50	NOV8a	PREKVACLPGSYTSGPDSSQPSLLLEMSSQEHETHADISTSQNHRPSCAETTEVTSASS					
	NOV8b	PREKVACLPGSYTSGPDSSQPSLLLEMSSQEHETHADISTSQNHRPSCAETTEVTSASS					
		1690	1700	1710	1720	1730	1740
55	NOV8a	AMENSPLSKVARHFHSPPIILSSPNMVNGLEHDLLDDETLNQYETSINAASLSSFSVDV					
	NOV8b	AMENSPLSKVARHFHSPPIILSSPNMVNGLEHDLLDDETLNQYETSINAASLSSFSVDV					
		1750	1760	1770	1780	1790	1800
60	NOV8a	PKNGESVLENLHISESQDLDLQLQPKKMIARRFIMAWFKEINKHNQGTHLRSKTEKEQPL					
	NOV8b	PKNGESVLENLHISESQDLDLQLQPKKMIARRFIMAWFKEINKHNQGTHLRSKTEKEQPL					
		1810	1820	1830	1840	1850	1860
65	NOV8a	MPARSPDLSKIQMVSSSSQKGVTVPHSPPPQPKPNLENKDLSSKKSPAEMLLTNGQAKCGPK					
	NOV8b	MPARSPDLSKIQMVSSSSQKGVTVPHSPPPQPKTNLENKDLSSKKSPAEMLLTNGQAKCGPK					
		1870	1880	1890	1900	1910	1920
70	NOV8a	LKRLSLKGKAKVNSEAPANAVKAGGTDHHRKPLISPQTSHKTLSKAVSQRHLHVADHEDPD					
	NOV8b	LKRLSLKGKAKVNSEAPANAVKAGGTDHHRKPLISPQTSHKTLSKAVSQRHLHVADHEDPD					

	1930	1940	1950	1960	1970	1980
5
NOV8a	RNTTAAPRSPQCVCLESKPPLATSGPLKPSVSDTSIRTFVSPLTSPKPVPEQGMWSRFHMA					
NOV8b	RNTTAAPRSPQCVCLESKPPLATSGPLKPSVSDTSIRTFVSPLTSPKPVPEQGMWSRFHMA					
	1990	2000	2010	2020	2030	2040
10
NOV8a	VLSEPDRGCPPTPKSPKCRAEGRAPRADSGPVSPAASRNGMSVAGNRQSEFRLASHVAAD					
NOV8b	VLSEPDRGCPPTPKSPKCRAEGRAPRADSGPVSPAASRNGMSVAGNRQSEFRLASHVAAD					
	2050	2060	2070	2080	2090	2100
15
NOV8a	TAQPRPTGEKGNNIMASDRLERTNQLKIVEISAEVSETVCGNPKAESDRRGGLAQQNC					
NOV8b	TAQPRPTGEKGNNIMASDRLERTNQLKIVEISAEVSETVCGNPKAESDRRGGLAQQNC					
	2110	2120	2130	2140	2150	2160
20
NOV8a	QEKEIRLYRQVAEESSTSHPFSSLPHASQAEQEMRSRSFSMAKLASSSSSLQTAIRKAEYS					
NOV8b	QEKEIRLYRQVAEESSTSHPFSSLPHASQAEQEMRSRSFSMAKLASSSSSLQTAIRKAEYS					
	2170	2180	2190	2200	2210	2220
25
NOV8a	QGKSSLMSDSRGVPRNSIPGGPSGEDHLYFTPRTYSMPAQFSSHFGREGHPPHSLG					
NOV8b	QGKSSLMSDSRGVPRNSIPGGPSGEDHLYFTPRTYSMPAQFSSHFGREGHPPHSLG					
	2230	2240	2250	2260	2270	2280
30
NOV8a	RSRDSQVPVTSSVVPEAKASRGGLPSILANGQGIYSVKPLLDTSRNLPATDEGDIISVQET					
NOV8b	RSRDSQVPVTSSVVPEAKASRGGLPSILANGQGIYSVKPLLDTSRNLPATDEGDIISVQET					
	2290	2300	2310	2320	2330	2340
35
NOV8a	SCLVTDKIKVTRRHYCQEQNWPHESTSFFSVKQRIKSSENLANADRPVAKSGASPFLSVS					
NOV8b	SCLVTDKIKVTRRHYCQEQNWPHESTSFFSVKQRIKSSENLANADRPVAKSGASPFLSVS					
	2350	2360	2370	2380	2390	2400
40
NOV8a	SKPIPIGRSSGSIVSGSLGHFGDAAARLLRRSLSSCSENQSEAGTLLPQMAKSPSIMTLT					
NOV8b	SKPIPIGRSSGSIVSGSLGHFGDAAARLLRRSLSSCSENQSEAGTLLPQMAKSPSIMTLT					
	2410	2420	2430	2440	2450	2460
45
NOV8a	ISRONQPETSSKGDSSELKKSLGPGLIPTPTMTLASPVKRMKSSVRHTQSPSPVSRSKLQE					
NOV8b	ISRONQPETSSKGDSSELKKSLGPGLIPTPTMTLASPVKRMKSSVRHTQSPSPVSRSKLQE					
	2470	2480	2490	2500	2510	2520
50
NOV8a	LRALSMPLDKLCSEDYSAGPSAVLFKTELEITPRRSPGPPAGGVSCPEKGNNRACPAGGS					
NOV8b	LRALSMPLDKLCSEDYSAGPSAVLFKTELEITPRRSPGPPAGGVSCPEKGNNRACPAGGS					
	2530	2540	2550	2560	2570	2580
55
NOV8a	GPKTSAAEPTSSASDICEAAQDLPFRRSNSVNLDQLLVSAQDQQLQSVLSSVGSKSTIL					
NOV8b	GPKTSAAEPTSSASDICEAAQDLPFRRSNSVNLDQLLVSAQDQQLQSVLSSVGSKSTIL					
	2590	2600	2610	2620	2630	2640
60
NOV8a	TLIQEAKAQSENEEDDVCFIVLNRKEGSGLGF SVAGGT DVEPKSITVHRVFSQGAASQEGT					
NOV8b	TLIQEAKAQSENEEDDVCFIVLNRKEGSGLGF SVAGGT DVEPKSITVHRVFSQGAASQEGT					
	2650	2660	2670	2680	2690	2700
65
NOV8a	MNRGDFLISVNGASLAGLAHGNVIKVHLHQALHKDALVVIKKGMQPRPSARQEPPTANG					
NOV8b	MNRGDFLISVNGASLAGLAHGNVIKVHLHQALHKDALVVIKKGMQPRPSARQEPPTANG					
	2710	2720	2730	2740	2750	2760
70
NOV8a	KGLLSRKTIPLPEGIGRSVAVHDALCVEVLKTSAGLGLSLDGKSSVTGDGPLVIKRVYK					
NOV8b	KGLLSRKTIPLPEGIGRSVAVHDALCVEVLKTSAGLGLSLDGKSSVTGDGPLVIKRVYK					

	2770	2780	2790	2800	2810	
NOV8a	(SEQ ID NO:25)
NOV8b	GGAAEQAGIIEAGDEILAIINGKPLVGLMHFDAWNIMKSVPPEGPVQLLIRKERNSS	GGAAEQAGIIEAGDEILAIINGKPLVGLMHFDAWNIMKSVPPEGPVQLLIRKERNSS				(SEQ ID NO:27)

5

Homologies to either of the above NOV8 proteins will be shared by the other NOV8 protein insofar as they are homologous to each other as shown above. Any reference to NOV8 is assumed to refer to both of the NOV8 proteins in general, unless otherwise noted.

The disclosed NOV8 polypeptide has homology to the amino acid sequences shown in 10 the BLASTP data listed in Table 8F.

Table 8F. BLAST results for NOV8

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 15295903 ref XP_043060.2	similar to NONE_RETURNED (R. norvegicus) [Homo sapiens]	1788	1712/1741 (98%)	1716/1741 (98%)	0.0
gi 2224541 dbj BAA20760.1 P	KIAA0300 [Homo sapiens]	1608	1608/1608 (100%)	1608/1608 (100%)	0.0
gi 12621106 ref NP_075229.1	PAPIN [Rattus norvegicus]	2766	1906/2843 (67%)	2147/2843 (75%)	0.0
gi 12751452 gb AAKO7661.1 AF338650_1	PDZ domain-containing protein AIPC [Homo sapiens]	2641	2256/2343 (96%)	2275/2343 (96%)	0.0
gi 12861607 dbj BAB32241.1	putative [Mus musculus]	364	314/387 (81%)	337/387 (86%)	e-157

The homology between these and other sequences is shown graphically in the ClustalW analysis shown in Table 8G. In the ClustalW alignment of the NOV8 protein, as 15 well as all other ClustalW analyses herein, the black outlined amino acid residues indicate regions of conserved sequence (*i.e.*, regions that may be required to preserve structural or functional properties), whereas non-highlighted amino acid residues are less conserved and can potentially be altered to a much broader extent without altering protein structure or function.

20

Table 8G. ClustalW Analysis of NOV8

- 1) Novel NOV8a (SEQ ID NO:25)
- 2) Novel NOV8b (SEQ ID NO:27)
- 3) gi|15295903|ref|XP_043060.2| similar to NONE_RETURNED (R. norvegicus) [Homo sapiens] (SEQ ID NO:60)
- 4) gi|2224541|dbj|BAA20760.1|P KIAA0300 [Homo sapiens] (SEQ ID NO:61)
- 5) gi|12621106|ref|NP_075229.1| PAPIN [Rattus norvegicus] (SEQ ID NO:62)
- 6) gi|12751452|gb|AAKO7661.1|AF338650_1 PDZ domain-containing protein AIPC [Homo sapiens] (SEQ ID NO:63)
- 7) gi|12861607|dbj|BAB32241.1| putative [Mus musculus] (SEQ ID NO:64)

10 20 30 40

5 NOV8a MPITQDNAVLHLPILLYQWLQNSLQEGGDGPEQRLCQAAIQLQEQYIQLNF
NOV8b MPITQDNAVLHLPILLYQWLQNSLQEGGDGPEQRLCQAAIQLQEQYIQLNF
gi|15295903|-----
gi|2224541|-----
gi|12621106|-----
gi|12751452|-----
gi|12861607|-----

60 70 80 90 100

10 NOV8a AVDESTVPPDHSPPEMEICTVYLTKELGDTETVGLSGFNIPVFGDYGEKR
NOV8b AVDESTVPPDHSPPEMEICTVYLTKELGDTETVGLSGFNIPVFGDYGEKR
gi|15295903|-----
gi|2224541|-----
gi|12621106|-----
gi|12751452|-----
gi|12861607|-----

110 120 130 140 150

15 NOV8a RGGKKRKTHQGPVLVDVGCIVWVTELRKNSPAGKSGKVRLRDEILSINQML
NOV8b RGGKKRKTHQGPVLVDVGCIVWVTELRKNSPAGKSGKVRLRDEILSINQML
gi|15295903|-----
gi|2224541|-----
gi|12621106|-----
gi|12751452|-----
gi|12861607|-----

160 170 180 190 200

20 NOV8a VGVDVSGASYLAEQCWNNGFFIYLIMLRRFKHKAHSTYNGNSSNSSEPGET
NOV8b VGVDVSGASYLAEQCWNNGFFIYLIMLRRFKHKAHSTYNGNSSNSSEPGET
gi|15295903|-----
gi|2224541|-----
gi|12621106|-----
gi|12751452|-----
gi|12861607|-----

210 220 230 240 250

25 NOV8a PTLELGDRATAKKGRTRKPGVISRPPIKPEESKGSAGCEVSSDPTEL
NOV8b PTLELGDRATAKKGRTRKPGVISRPPIKPEESKGSAGCEVSSDPTEL
gi|15295903|-----
gi|2224541|-----
gi|12621106|-----
gi|12751452|-----
gi|12861607|-----

260 270 280 290 300

30 NOV8a ENGLDPELGNGHVFQLENGPDSLKEVAGPHILERSEVDRGTEHRIPKTDA
NOV8b ENGLDPELGNGHVFQLENGPDSLKEVAGPHILERSEVDRGTEHRIPKTDA
gi|15295903|-----
gi|2224541|-----
gi|12621106|-----
gi|12751452|-----
gi|12861607|-----

310 320 330 340 350

35 NOV8a LTTSNDKRRFSKGKTDQFQS SDCLARSKEEVGRIWKMELLKESDGLGIQV
NOV8b LTTSNDKRRFSKGKTDQFQS SDCLARSKEEVGRIWKMELLKESDGLGIQV
gi|15295903|-----
gi|2224541|-----
gi|12621106|-----
gi|12751452|-----
gi|12861607|-----

360 370 380 390 400

40 NOV8a SGGRGSKRSPHAIVVTQVKGGAAHRLRDGRLSLGDELLVINGHLLVGLS
NOV8b SGGRGSKRSPHAIVVTQVKGGAAHRLRDGRLSLGDELLVINGHLLVGLS
gi|15295903|-----
gi|2224541|-----
gi|12621106|-----

5	gi 2224541	-----				
	gi 12621106	-----				
	gi 12751452	LEVNSVNVRHAALSKVHAILSKCP-----	VSEQEMDE			
	gi 12861607	-----				
		810	820	830	840	850
10	NOV8a	VIARSTYQESKEANSSPGLTVISIGCPLLQQDSLISESELSQYFAHDVP				
	NOV8b	VIARSTYQESKEANSSPGLTPLKS-PSIACKDSLISESELSQYFAHDVP				
	gi 15295903	-----				
	gi 2224541	-----				
	gi 12621106	-----				
	gi 12751452	VIARSTYQESKEANSSPGLTPLKS-PSIACKDSLISESELSQYFAHDVP				
	gi 12861607	-----				
		860	870	880	890	900
20	NOV8a	GPLSDFMVGSEDEDHPGSGCSTSEEGSLPPSTSTHKEPGKPRANSLVTL				
	NOV8b	GPLSDFMVGSEDEDHPGSGCSTSEEGSLPPSTSTHKEPGKPRANSLVTL				
	gi 15295903	-----				
	gi 2224541	-----				
	gi 12621106	-----				
	gi 12751452	GPLSDFMVGSHDBDHPGSGCSTSEEGSLPP--STSSEPGKPRANSLVTL				
	gi 12861607	-----				
		910	920	930	940	950
30	NOV8a	GSHRASGLFHKVTVARQASLPGSPQALRNPLLQRKVGCYDANDASDEE				
	NOV8b	GSHRASGLFHKVTVARQASLPGSPQALRNPLLQRKVGCYDANDASDEE				
	gi 15295903	-----				
	gi 2224541	-----				
	gi 12621106	-----				
	gi 12751452	GSHRASGLFHKVTVARQASLPGSPQALRNPLLQRKVGCYDANDASDEE				
	gi 12861607	-----				
		960	970	980	990	1000
40	NOV8a	EFDREGDCISLPGALPGPIRPLSEDDPRRVSISSSKGMVDVHNQEERPRKT				
	NOV8b	EFDREGDCISLPGALPGPIRPLSEDDPRRVSISSSKGMVDVHNQEERPRKT				
	gi 15295903	-----	MIRFMQPT			
	gi 2224541	-----				
	gi 12621106	-----	MPIITQDN	ALLHLP		
	gi 12751452	EFDREGDCISLPGALPGPIRPLSEDDPRRVSISSSKGMVDVHNQEERPRKT				
	gi 12861607	-----				
		1010	1020	1030	1040	1050
50	NOV8a	LVSKAISAPLLGSSVDLEESIPEGMVDAAASYAANLTDSEAEAPKGSPGSWW				
	NOV8b	LVSKAISAPLLGSSVDLEESIPEGMVDAAASYAANLTDSEAEAPKGSPGSWW				
	gi 15295903	--RTFQRPPRGA--LGAGGRRNCQDQVAHPNWNTQEVQTPR				
	gi 2224541					
	gi 12621106	LLYEWLQLNSLRGGDSPEQLCQAAIQKLQBYIQLNLAQDESTVPPDHSP				
	gi 12751452	LVSKAISAPLLGSSVDLEESIPEGMVDAAASYAANLTDSEAEAPKGSPGSWW				
	gi 12861607	-----				
		1060	1070	1080	1090	1100
60	NOV8a	KKELSGSSSAPKLEYTVRTDTQSPTNTGSPSSPOQSEGGLGSRHRPVARV				
	NOV8b	KKELSGSSSAPKLEYTVRTDTQSPTNTGSPSSPOQSEGGLGSRHRPVARV				
	gi 15295903	-----	VRRTLGPVPPSRKVKAWAPGTDQWPGV			
	gi 2224541					
	gi 12621106	PEMBEICTVYLTKQLGDTETVGLSFGNIPVFGDYGENRRGGKKRKTHQGPV				
	gi 12751452	KKELSGSSSAPKLEYTVRTDTQSPTNTGSPSSPOQSEGGLGSRHRPVARV				
	gi 12861607	-----				
		1110	1120	1130	1140	1150
70	NOV8a	SPHCKRSEAAPKPGSQTVNLIGRANDPCDLDSRVQATSVKVTVIGCOPG				
	NOV8b	SPHCKRSEAAPKPGSQTVNLIGRANDPCDLDSRVQATSVKVTVIGCOPG				
	gi 15295903	-----	SPHCKRSEAAPKPGSQTVNLIGRANDPCDLDSRVQATSVKVTVIGCOPG			
	gi 2224541	-----				
	gi 12621106	LDVGCINVTEALKNSPAAGKSCGVRLRDEILSINGQIMVGVDVTGISMIAE				
	gi 12751452	SPHCKRSEAAPKPGSQTVNLIGRANDPCDLDSRVQATSVKVTVIGCOPG				
	gi 12861607	-----				
		1160	1170	1180	1190	1200
75	NOV8a	GAVEK--ESLGKTTGDACVSTSCELASALESHODASHILPENLPKAASBL				

NOV8b GAVEK---ES[E]GKLTIGDACVSTSCELASALS[SHLDASHL]TENLPKAASEL
 gi|15295903| GAVEKLCQESI[GKLITGDACVSTSCELASALS[SHLDASHL]TENLPKAASEL
 gi|2224541| -----
 5 gi|12621106| QCWNG-CFIVIIMI[RFFKQKAHVITYNGN]GNSS[EPGTP]TLELGDQTSKK
 gi|12751452| GAVEKLCQESI[GKLITGDACVSTSCELASALS[SHLDASHL]TENLPKAASEL
 gi|12861607| -----MLRFFKQKAHLTYNGN]GNSS[EPGTP]TLELGDQTSKK

	1210	1220	1230	1240	1250
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NOV8a GQQPMTELDSSSDLISSPGKGGAAHPDPSKTSVDTG[VSRPENPSOPASF
 NOV8b GQQPMTELDSSSDLISSPGKGGAAHPDPSKTSVDTG[VSRPENPSOPASF
 gi|15295903| GQQPMT-----SSDLISSPGKGGAAHPDPSKTSVDTG[VSRPENPSOPASF
 gi|2224541| -----SSDLISSPGKGGAAHPDPSKTSVDTG[VSRPENPSOPASF
 15 gi|12621106| GKRTRK-----FGVISRPEISKTPEDSKR[SSGCC]TADDPNSELENG-----
 gi|12751452| GKRTRK-----SSDLISSPGKGGAAHPDPSKTSVDTG[VSRPENPSOPASF
 gi|12861607| GKRTRK-----FGVISRPAIIKAPEDSKR[SSGCC]TADDPNSELENG-----

	1260	1270	1280	1290	1300
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20 NOV8a RV[KCKARSPVRLPHEGSPSPGEKAAPPDYSKTRSASETSTPHNTRRVA
 NOV8b RV[KCKARSPVRLPHEGSPSPGEKAAPPDYSKTRSASETSTPHNTRRVA
 gi|15295903| RV[KCKARSPVRLPHEGSPSPGEKAAPPDYSKTRSASETSTPHNTRRVA
 gi|2224541| -----ADPE[LGN]GHAFELENG[PNSLKDVA]GP---HLERSEAD[E]VELRVP[X]TE
 25 gi|12621106| RV[KCKARSPVRLPHEGSPSPGEKAAPPDYSKTRSASETSTPHNTRRVA
 gi|12751452| RV[KCKARSPVRLPHEGSPSPGEKAAPPDYSKTRSASETSTPHNTRRVA
 gi|12861607| -----TDS[LGN]GHAFELENG[PNSLKDVA]GP---HLERSEAD[R]EAE[L]RVP[X]TE

	1310	1320	1330	1340	1350
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30 NOV8a ALRGAGPGAEGMT[PAGAVLP]GDP[PLTSQ]EQ[ORQ]CAP[PNH]SKALEMTG[I]HAPE
 NOV8b ALRGAGPGAEGMT[PAGAVLP]GDP[PLTSQ]EQ[ORQ]CAP[PNH]SKALEMTG[I]HAPE
 gi|15295903| ALRGAGPGAEGMT[PAGAVLP]GDP[PLTSQ]EQ[ORQ]CAP[PNH]SKALEMTG[I]HAPE
 gi|2224541| -----PLSDSND[KR]RF[E]K[GK]TID[F]QS[D]CLAR[EV]RIWKMELL[K]ESD[SL]G[I]QV
 35 gi|12621106| ALRGAGPGAEGMT[PAGAVLP]GDP[PLTSQ]EQ[ORQ]CAP[PNH]SKALEMTG[I]HAPE
 gi|12751452| ALRGAGPGAEGMT[PAGAVLP]GDP[PLTSQ]EQ[ORQ]CAP[PNH]SKALEMTG[I]HAPE
 gi|12861607| -----PLSDSND[KR]RF[E]K[GK]TIN[F]QS[D]CLAR[EV]RIWKMELL[K]ESD[SL]G[I]QV

	1360	1370	1380	1390	1400
--	------	------	------	------	------

40 NOV8a SSQEPSLLEGADS[VSSRA]PQASL[SM]LPSTDNTKEACGHVSGHC[CPGG]SRE
 NOV8b SSQEPSLLEGADS[VSSRA]PQASL[SM]LPSTDNTKEACGHVSGHC[CPGG]SRE
 gi|15295903| SSQEPSLLEGADS[VSSRA]PQASL[SM]LPSTDNTKEACGHVSGHC[CPGG]SRE
 gi|2224541| -----SSGRGS[KRS]PHAI[V]TQVK[G]GGAAHRDGRLS[LG]DELLV[CH]LVL[SL]HE
 45 gi|12621106| EAVAI[ERS]ATGM[V]QLVV[SKML]GSEE[ODV]SS[EE]SKGN[LE]SPKQGNCK
 gi|12751452| SSQEPSLLEGADS[VSSRA]PQASL[SM]LPSTDNTKEACGHVSGHC[CPGG]SRE
 gi|12861607| SGRGS[KRS]PHAI[V]TQVK[G]GGAAHRDGRLS[LG]DELLV[CH]LVL[SL]HE

	1410	1420	1430	1440	1450
--	------	------	------	------	------

50 NOV8a SPVT[D]IDSFI[KELDASA]ARSP-----SSQTGDSG[QEG]SAQGH[PAGA]GGGSRE
 NOV8b SPVT[D]IDSFI[KELDASA]ARSP-----SSQTGDSG[QEG]SAQGH[PAGA]GGGSRE
 gi|15295903| SPVT[D]IDSFI[KELDASA]ARSP-----SSQTGDSG[QEG]SAQGH[PAGA]GGGSRE
 gi|2224541| -----SPVT[D]IDSFI[KELDASA]ARSP-----SSQTGDSG[QEG]SAQGH[PAGA]GGGSRE
 55 gi|12621106| EAVAI[ERS]ATGM[V]QLVV[SKML]GSEE[ODV]SS[EE]SKGN[LE]SPKQGNCK
 gi|12751452| SPVT[D]IDSFI[KELDASA]ARSP-----SSQTGDSG[QEG]SAQGH[PAGA]GGGSRE
 gi|12861607| EAVAI[ERS]ATGM[V]QLVV[SKML]GSEE[ODV]SS[EE]SKGN[LE]SPKQGNCK

	1460	1470	1480	1490	1500
--	------	------	------	------	------

60 NOV8a CRAE[VPGQQTSS]P[RRA]AAGA[PAY]PQWA[SQF]SVLDSIN[PDKHFT]VNKNF
 NOV8b CRAE[VPGQQTSS]P[RRA]AAGA[PAY]PQWA[SQF]SVLDSIN[PDKHFT]VNKNF
 gi|15295903| CRAE[VPGQQTSS]P[RRA]AAGA[PAY]PQWA[SQF]SVLDSIN[PDKHFT]VNKNF
 gi|2224541| -----CRAE[VPGQQTSS]P[RRA]AAGA[PAY]PQWA[SQF]SVLDSIN[PDKHFT]VNKNF
 65 gi|12621106| T[K]S[R]L[S]G[V]H[R]L[ES]V[E]Y[N]LM[V]RN[G]D[P]I[R]M[L]E[V]S[R]D[G][K]H[S]I[P]ELL
 gi|12751452| CRAE[VPGQQTSS]P[RRA]AAGA[PAY]PQWA[SQF]SVLDSIN[PDKHFT]VNKNF
 gi|12861607| M[K]S[R]L[S]G[V]H[R]L[ES]V[E]Y[N]LM[V]RN[G]D[P]I[R]M[L]E[V]S[R]D[G][K]H[S]I[P]ELL

	1510	1520	1530	1540	1550
--	------	------	------	------	------

70 NOV8a LSN-[YSRNFSSF]HEDSTSLSGLGDST-----EPSLSSMYG-----
 NOV8b LSN-[YSRNFSSF]HEDSTSLSGLGDST-----EPSLSSMYG-----
 gi|15295903| LSN-[YSRNFSSF]HEDSTSLSGLGDST-----EPSLSSMYG-----
 gi|2224541| LSN-[YSRNFSSF]HEDSTSLSGLGDST-----EPSLSSMYG-----
 75 gi|12621106| DSTGT[SQE]H[V]IKXSTRSLSTTHVE[P]WRLIR[P]S/[S]H[G]LYKEKGKGLG
 gi|12751452| LSN-[YSRNFSSF]HEDSTSLSGLGDST-----EPSLSSMYG-----
 gi|12861607| DSTGT[SQE]H[V]IKXSTRSLSTTHVE[P]WRLIR[P]S/[S]H[G]

	1560	1570	1580	1590	1600
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		1960	1970	1980	1990	2000	
5	NOV8a					
	NOV8b	----- ----- ----- ----- ----- ----- -----					
	g1 15295903	----- ----- ----- ----- ----- ----- -----					
	g1 2224541	----- ----- ----- ----- ----- ----- -----					
	g1 12621106	TRPALTTSSKSIDVNQK3ERLQPLVKACSVPLLGSSLDEHSILNGAG					
10	g1 12751452	----- ----- ----- ----- ----- ----- -----					
	g1 12861607	----- ----- ----- ----- ----- ----- -----					
			2010	2020	2030	2040	2050
15	NOV8a					
	NOV8b	----- ----- ----- ----- ----- ----- -----					
	g1 15295903	----- ----- ----- ----- ----- ----- -----					
	g1 2224541	----- ----- ----- ----- ----- ----- -----					
	g1 12621106	GTPPKVASLPGSGETPKNGPRGSGRKEMSGSRSSPKLEYRVPTDTQSPRS					
20	g1 12751452	----- ----- ----- ----- ----- ----- -----					
	g1 12861607	----- ----- ----- ----- ----- ----- -----					
			2060	2070	2080	2090	2100
25	NOV8a					
	NOV8b	----- ----- ----- ----- ----- ----- -----					
	g1 15295903	----- ----- ----- ----- ----- ----- -----					
	g1 2224541	----- ----- ----- ----- ----- ----- -----					
	g1 12621106	PENHTSPPQKSENLVSRHKPVARISPHYKRSDAEEAPGGTANGPCAQDLK					
30	g1 12751452	----- ----- ----- ----- ----- ----- -----					
	g1 12861607	----- ----- ----- ----- ----- ----- -----					
			2110	2120	2130	2140	2150
35	NOV8a					
	NOV8b	----- ----- ----- ----- ----- ----- -----					
	g1 15295903	----- ----- ----- ----- ----- ----- -----					
	g1 2224541	----- ----- ----- ----- ----- ----- -----					
	g1 12621106	VQASPVKDPVTSRQPGGTAEKELRGNPTPGDSSVPTNCGPASTPCHPNIG					
40	g1 12751452	----- ----- ----- ----- ----- ----- -----					
	g1 12861607	----- ----- ----- ----- ----- ----- -----					
			2160	2170	2180	2190	2200
45	NOV8a					
	NOV8b	----- ----- ----- ----- ----- ----- -----					
	g1 15295903	----- ----- ----- ----- ----- ----- -----					
	g1 2224541	----- ----- ----- ----- ----- ----- -----					
	g1 12621106	LPTENPQGAAPFCGPHPGTGWDGSSEHLCSPGKSRREVHPDSSETPTVAEQ					
50	g1 12751452	----- ----- ----- ----- ----- ----- -----					
	g1 12861607	----- ----- ----- ----- ----- ----- -----					
			2210	2220	2230	2240	2250
55	NOV8a					
	NOV8b	----- ----- ----- ----- ----- ----- -----					
	g1 15295903	----- ----- ----- ----- ----- ----- -----					
	g1 2224541	----- ----- ----- ----- ----- ----- -----					
	g1 12621106	VRQOPESLSQPVSRTSEPESQGISKMKPPSQRCVSPREKASTPPDSSRAW					
60	g1 12751452	----- ----- ----- ----- ----- ----- -----					
	g1 12861607	----- ----- ----- ----- ----- ----- -----					
			2260	2270	2280	2290	2300
65	NOV8a					
	NOV8b	----- ----- ----- ----- ----- ----- -----					
	g1 15295903	----- ----- ----- ----- ----- ----- -----					
	g1 2224541	----- ----- ----- ----- ----- ----- -----					
	g1 12621106	AAPGDSSPSTRRIAVPMSTGAAPATAIPQASLWSQERSRGGLSGPSKG					
70	g1 12751452	----- ----- ----- ----- ----- ----- -----					
	g1 12861607	----- ----- ----- ----- ----- ----- -----					
			2310	2320	2330	2340	2350
75	NOV8a					
	NOV8b	----- ----- ----- ----- ----- ----- -----					
	g1 15295903	----- ----- ----- ----- ----- ----- -----					
	g1 2224541	----- ----- ----- ----- ----- ----- -----					
	g1 12621106	KELCIPKSLKDALLEDTAPASGKMSHASSPSGPVATERTLGSOPENPVT					

gi 12751452	-----
gi 12861607	-----
	2360 2370 2380 2390 2400
5 NOV8a
NOV8b	-----
gi 15295903	-----
gi 2224541	-----
10 gi 12621106	DIDNFIEEASEARLSQSPQKADCRAGDTFESQPPGGAGSSSHIAQMVR
gi 12751452	-----
gi 12861607	-----
	2410 2420 2430 2440 2450
15 NOV8a
NOV8b	-----
gi 15295903	-----
gi 2224541	-----
20 gi 12621106	SDQTSSPRKTGGTGSPPPQQNALQPSVLDSIHPPDKHLAVNKTFLNNSRN
gi 12751452	-----
gi 12861607	-----
	2460 2470 2480 2490 2500
25 NOV8a
NOV8b	-----
gi 15295903	-----
gi 2224541	-----
30 gi 12621106	FSNFHEDSIISLGPFGSSEPSFSMVGNAEDSSSDPESLAEDPCAAARN
gi 12751452	-----
gi 12861607	-----
	2510 2520 2530 2540 2550
35 NOV8a	WSPPRSRVSLHKEPDSEBEEQIEICSTRGCPNPSSPAHLPTQAAICPA
NOV8b	WSPPRSRVSLHKEPDSEBEEQIEICSTRGCPNPSSPAHLPTQAAICPA
gi 15295903	WSPPRSRVSLHKEPDSEBEEQIEICSTRGCPNPSSPAHLPTQAAICPA
gi 2224541	WSPPRSRVSLHKEPDSEBEEQIEICSTRGCPNPSSPAHLPTQAAICPA
40 gi 12621106	WSPPLSPESPKGSSESEPRIEICSTDSCPCTP-----VATAPPPTOVA
gi 12751452	WSPPRSRVSLHKEPDSEBEEQIEICSTRGCPNPSSPAHLPTQAAICPA
gi 12861607	-----
	2560 2570 2580 2590 2600
45 NOV8a	SAKVLSLKYSTPRESVASPREKACLP-GSYTSGPDSSQPSLLEMSSQE
NOV8b	SAKVLSLKYSTPRESVASPREKACLP-GSYTSGPDSSQPSLLEMSSQE
gi 15295903	SAKVLSLKYSTPRESVASPREKACLP-GSYTSGPDSSQPSLLEMSSQE
gi 2224541	SAKVLSLKYSTPRESVASPREKACLP-GSYTSGPDSSQPSLLEMSSQE
50 gi 12621106	LCPVLFVQORAVCFPVGIDCERACFVPGASRITSPIDSSQPSLLEMSSQE
gi 12751452	SAKVLSLKYSTPRESVASPREKACLP-GSYTSGPDSSQPSLLEMSSQE
gi 12861607	-----
	2610 2620 2630 2640 2650
55 NOV8a	HETHADISTSQNHRPSCAETTEVTASSAMENSPLSKVARHFHSPPIL
NOV8b	HETHADISTSQNHRPSCAETTEVTASSAMENSPLSKVARHFHSPPIL
gi 15295903	HETHADISTSQNHRPSCAETTEVTASSAMENSPLSKVARHFHSPPIL
gi 2224541	HETHADISTSQNHRPSCAETTEVTASSAMENSPLSKVARHFHSPPIL
60 gi 12621106	PETMASINAQNMPVCREGIMIVTSISSLNEDPSOSQTRHCRNAPYIL
gi 12751452	HETHADISTSQNHRPSCAETTEVTASSAMENSPLSKVARHFHSPPIL
gi 12861607	-----
	2660 2670 2680 2690 2700
65 NOV8a	SSPNMVNGLEHDLLDDETLNQYETSINAAAALSSSFVDPVKNGESVLENL
NOV8b	SSPNMVNGLEHDLLDDETLNQYETSINAAAALSSSFVDPVKNGESVLENL
gi 15295903	SSPNMVNGLEHDLLDDETLNQYETSINAAAALSSSFVDPVKNGESVLENL
gi 2224541	SSPNMVNGLEHDLLDDETLNQYETSINAAAALSSSFVDPVKNGESVLENL
70 gi 12621106	GNPLMVNDLGRDLLDEGAKPEGAAAASVMSVFLGAKGPKNGFAVIALD
gi 12751452	SSPNMVNGLEHDLLDDETLNQYETSINAAAALSSSFVDPVKNGESVLENL
gi 12861607	-----
	2710 2720 2730 2740 2750
75 NOV8a	HISESDQLDDLLQPKMIAARRPIMAWFKEINKHNGTHLRSKTEKEQPLM
NOV8b	HISESDQLDDLLQPKMIAARRPIMAWFKEINKHNGTHLRSKTEKEQPLM
gi 15295903	HISESDQLDDLLQPKMIAARRPIMAWFKEINKHNGTHLRSKTEKEQPLM

5	gi 2224541	HISESDQLDDLLQKPKMIARRPIMAWFKEINKHNOGTHLRSKTEKEQPLM
	gi 12621106	HIAERGNLEDLQKPKIISRRPITAWFKEINKHNOGTHLRSKTEKEQPLM
	gi 12751452	HISESDQLDDLLQKPKMIARRPIMAWFKEINKHNOGTHLRSKTEKEQPLM
	gi 12861607	-----
		2760 2770 2780 2790 2800
10	NOV8a	PARSPDSKIQMVSSSQKKGVTVPHSPPPQPKTNLENKDLSSLKSPAEMLLTN
	NOV8b	PARSPDSKIQMVSSSQKKGVTVPHSPPPQPKTNLENKDLSSLKSPAEMLLTN
	gi 15295903	PARSPDSKIQMVSSSQKKGVTVPHSPPPQPKTNLENKDLSSLKSPAEMLLTN
	gi 2224541	PARSPDSKIQMVSSSQKKGVTVPHSPPPQPKTNLENKDLSSLKSPAEMLLTN
	gi 12621106	LAEGPCSKIAVMVNTCHRKGTVTPKSPPSRQKSENKDLPKSPWPTLN
	gi 12751452	PARSPDSKIQMVSSSQKKGVTVPHSPPPQPKTNLENKDLSSLKSPAEMLLTN
	gi 12861607	-----
		2810 2820 2830 2840 2850
15	NOV8a	GOKAKCGPKLKRLSLKGKAKVNSEAAPAANAVKAGGTDHRKPLISPQTSHK
	NOV8b	GOKAKCGPKLKRLSLKGKAKVNSEAAPAANAVKAGGTDHRKPLISPQTSHK
	gi 15295903	GOKAKCGPKLKRLSLKGKAKVNSEAAPAANAVKAGGTDHRKPLISPQTSHK
	gi 2224541	GOKAKCGPKLKRLSLKGKAKVNSEAAPAANAVKAGGTDHRKPLISPQTSHK
	gi 12621106	COKPKOSPILKRLNSKGKAESP-BVPVAISTKSRNDHRLPSPQASHK
	gi 12751452	GOKAKCGPKLKRLSLKGKAKVNSEAAPAANAVKAGGTDHRKPLISPQTSHK
	gi 12861607	-----
		2860 2870 2880 2890 2900
20	NOV8a	TLSKAVSQRHLHVADHEDPDRTNTAAPRSFCVCLESKPPLATSGPLKPSVS
	NOV8b	TLSKAVSQRHLHVADHEDPDRTNTAAPRSFCVCLESKPPLATSGPLKPSVS
	gi 15295903	TLSKAVSQRHLHVADHEDPDRTNTAAPRSFCVCLESKPPLATSGPLKPSVS
	gi 2224541	TLSKAVSQRHLHVADHEDPDRTNTAAPRSFCVCLESKPPLATSGPLKPSVS
	gi 12621106	MESKAVSQRHLHVADHEDPDRTNTAAPRSFCVCLESKPPLATSGPLKPSVS
	gi 12751452	TLSKAVSQRHLHVADHEDPDRTNTAAPRSFCVCLESKPPLATSGPLKPSVS
	gi 12861607	-----
		2910 2920 2930 2940 2950
25	NOV8a	DTSIRTFVSPLTSPKPVPEOGMWSRFHMAVLSEPDRCPTTPKSPKCRAE
	NOV8b	DTSIRTFVSPLTSPKPVPEOGMWSRFHMAVLSEPDRCPTTPKSPKCRAE
	gi 15295903	DTSIRTFVSPLTSPKPVPEOGMWSRFHMAVLSEPDRCPTTPKSPKCRAE
	gi 2224541	DTSIRTFVSPLTSPKPVPEOGMWSRFHMAVLSEPDRCPTTPKSPKCRAE
	gi 12621106	DTSIRTFVSPLTSPKPVPEOGMWSRFHMAVLSEPDRCPTTPKSPKCRAE
	gi 12751452	DTSIRTFVSPLTSPKPVPEOGMWSRFHMAVLSEPDRCPTTPKSPKCRAE
	gi 12861607	-----
		2960 2970 2980 2990 3000
30	NOV8a	GRAPRADSGPVSPAASRNGMSVAGNRQSE-----PRLASHVAADTAQPRPTG
	NOV8b	GRAPRADSGPVSPAASRNGMSVAGNRQSE-----PRLASHVAADTAQPRPTG
	gi 15295903	GRAPRADSGPVSPAASRNGMSVAGNRQSE-----PRLASHVAADTAQPRPTG
	gi 2224541	GRAPRADSGPVSPAASRNGMSVAGNRQSE-----PRLASHVAADTAQPRPTG
	gi 12621106	SKAPAHMSGASPPASRASLACAGTROSEQFTIGRAIDLIVSFATOPQQGIC
	gi 12751452	GRAPRADSGPVSPAASRNGMSVAGNRQSE-----PRLASHVAADTAQPRPTG
	gi 12861607	-----
		3010 3020 3030 3040 3050
35	NOV8a	EKGGNIMASDRLERTNQLKIVEISAEEAVSETVCGNKPAAESDRRGGLAOG
	NOV8b	EKGGNIMASDRLERTNQLKIVEISAEEAVSETVCGNKPAAESDRRGGLAOG
	gi 15295903	EKGGNIMASDRLERTNQLKIVEISAEEAVSETVCGNKPAAESDRRGGLAOG
	gi 2224541	EKGGNIMASDRLERTNQLKIVEISAEEAVSETVCGNKPAAESDRRGGLAOG
	gi 12621106	EKGAEKKVSDPPORTINQLKIVEISSERVKNAKGDRPFESDRKGGLAOG
	gi 12751452	EKGGNIMASDRLERTNQLKIVEISAEEAVSETVCGNKPAAESDRRGGLAOG
	gi 12861607	-----
		3060 3070 3080 3090 3100
40	NOV8a	NCQEKESEIRLYRQVAEESSTSHPSSLPSHASQAEOEMRSFSMAKLAASSSS
	NOV8b	NCQEKESEIRLYRQVAEESSTSHPSSLPSHASQAEOEMRSFSMAKLAASSSS
	gi 15295903	NCQEKESEIRLYRQVAEESSTSHPSSLPSHASQAEOEMRSFSMAKLAASSSS
	gi 2224541	NCQEKESEIRLYRQVAEESSTSHPSSLPSHASQAEOEMRSFSMAKLAASSSS
	gi 12621106	NCQEKSMAIRLR-QSEESSPEHTPFFPSQASQVBRENTWSFSMAKPAASSSS
	gi 12751452	NCQEKESEIRLYRQVAEESSTSHPSSLPSHASQAEOEMRSFSMAKLAASSSS
	gi 12861607	-----
		3110 3120 3130 3140 3150
45	NOV8a	S-LQTAIRKABYSQGKSSLMSDSRGVPRNSIPGGPSGEDHLYFTPRPATR

5	NOV8b gi 15295903 S_LQTAIRKAEYSQGKSSLMSDSRGVPRNSIPCGGPSGEDHLYFTPREATR gi 2224541 S_LQTAIRKAEYSQGKSSLMSDSRGVPRNSIPCGGPSGEDHLYFTPREATR gi 12621106 S_LQTAIRKAEYSQGKSSLMSDSRGVPRNSIPCGGPSGEDHLYFTPREATR gi 12751452 S_LQTAIRKAEYSQGKSSLMSDSRGVPRNSIPCGGPSGEDHLYFTPREATR gi 12861607 S_LQTAIRKAEYSQGKSSLMSDSRGVPRNSIPCGGPSGEDHLYFTPREATR
	3160 3170 3180 3190 3200
10	NOV8a NOV8b gi 15295903 TYSMPAQSFSHFGREGHPPHSGLRSRDSQVPVTSSVVPEAKASRGGLPSL gi 2224541 TYSMPAQSFSHFGREGHPPHSGLRSRDSQVPVTSSVVPEAKASRGGLPSL gi 12621106 TYSMPAQSFSHFGREGHPPHSGLRSRDSQVPVTSSVVPEAKASRGGLPSL gi 12751452 TYSMPAQSFSHFGREGHPPHSGLRSRDSQVPVTSSVVPEAKASRGGLPSL gi 12861607
	3210 3220 3230 3240 3250
15	NOV8a NOV8b gi 15295903 ANGQGIYSVKPLLDTSRNLPATDEGDIISVQETSCLVTDKIKVTRRHYC gi 2224541 ANGQGIYSVKPLLDTSRNLPATDEGDIISVQETSCLVTDKIKVTRRHYC gi 12621106 ANGQGIYSVKPLLDTSRNLPATDEGDIISVQETSCLVTDKIKVTRRHYC gi 12751452 ANGQGIYSVKPLLDTSRNLPATDEGDIISVQETSCLVTDKIKVTRRHYC gi 12861607
	3260 3270 3280 3290 3300
20	NOV8a NOV8b gi 15295903 EQNWPHESTSF SVKQRIKSFENLANADRPVAKGASPFLSVSSKPIGR gi 2224541 EQNWPHESTSF SVKQRIKSFENLANADRPVAKGASPFLSVSSKPIGR gi 12621106 EQNWPHESTSF SVKQRIKSFENLANADRPVAKGASPFLSVSSKPIGR gi 12751452 EQNWPHESTSF SVKQRIKSFENLANADRPVAKGASPFLSVSSKPIGR gi 12861607
	3310 3320 3330 3340 3350
25	NOV8a NOV8b gi 15295903 RSSGSIVSGSLCHPGDAAARLLRRSLSSCSENQSEAGTLLPQMAKSPSIM gi 2224541 RSSGSIVSGSLCHPGDAAARLLRRSLSSCSENQSEAGTLLPQMAKSPSIM gi 12621106 RSSGSIVSGSLCHPGDAAARLLRRSLSSCSENQSEAGTLLPQMAKSPSIM gi 12751452 RSSGSIVSGSLCHPGDAAARLLRRSLSSCSENQSEAGTLLPQMAKSPSIM gi 12861607
	3360 3370 3380 3390 3400
30	NOV8a NOV8b gi 15295903 TTLTISRQNPPETSSKGSDSELKKSLGPLGIPPTPTMTLASPVKRNKSSVRH gi 2224541 TTLTISRQNPPETSSKGSDSELKKSLGPLGIPPTPTMTLASPVKRNKSSVRH gi 12621106 TTLTISRQNPPETSSKGSDSELKKSLGPLGIPPTPTMTLASPVKRNKSSVRH gi 12751452 TTLTISRQNPPETSSKGSDSELKKSLGPLGIPPTPTMTLASPVKRNKSSVRH gi 12861607
	3410 3420 3430 3440 3450
35	NOV8a NOV8b gi 15295903 TQPSPVSRSKLQELRALSMPLDKLCS-EDYSAAGPSAVLFKTELEITPRR gi 2224541 TQPSPVSRSKLQELRALSMPLDKLCS-EDYSAAGPSAVLFKTELEITPRR gi 12621106 TQPSPVSRSKLQELRALSMPLDKLCS-EDYSAAGPSAVLFKTELEITPRR gi 12751452 AQPSPVSRSKLQELRALSMPLDKLCS-EDYSAAGPSAVLFKTELEITPRR gi 12861607
	3460 3470 3480 3490 3500
40	NOV8a NOV8b gi 15295903 SPGPBPAGG-----VSCPEKGGNRACPGGSGPKTSAAET gi 2224541 SPGPBPAGG-----VSCPEKGGNRACPGGSGPKTSAAET gi 12621106 SPGPBPAGG-----VSCPEKGGNRACPGGSGPKTSAAET gi 12751452 SKGSQATSPAGSPARGHADFNGSTLSCPMNGGTRAYTKGSPPASBPAI gi 12861607
	3510 3520 3530 3540 3550

	NOV8a	PSSASDTGEAAQDLFRRRSWSVLNLDQLLVSAQGDQQLRQSVLSSVGSKSTI
	NOV8b	PSSASDTGEAAQDLFRRRSWSVLNLDQLLVSAQGDQQLRQSVLSSVGSKSTI
5	gi 15295903	PSSASDTGEAAQDLFRRRSWSVLNLDQLLVSAQGDQQLRQSVLSSVGSKSTI
	gi 2224541	AIGSREEGESVWATPSGRWSWVLSDRILLASVGNQORLQGILSIVGSKSPI
	gi 12621106	PSSASDTGEAAQDLFRRRSWSVLNLDQLLVSAQGDQQLRQSVLSSVGSKSTI
	gi 12751452	
	gi 12861607	
10		3560 3570 3580 3590 3600
	NOV8a	LTLIQEAKAQAQSENEDDVCFIVLNRKEGSGLGFSVAGGTDVEPKSITVHRV
	NOV8b	LTLIQEAKAQAQSENEDDVCFIVLNRKEGSGLGFSVAGGTDVEPKSITVHRV
15	gi 15295903	LTLIQEAKAQAQSENEDDVCFIVLNRKEGSGLGFSVAGGTDVEPKSITVHRV
	gi 2224541	LTLIQEAKAQAQSENEDDVCFIVLNRKEGSGLGFSVAGGTDVEPKSITVHRV
	gi 12621106	LTLIQEAKAQAQSENEDDVCFIVLNRKEGSGLGFSVAGGTDVEPKSITVHRV
	gi 12751452	LTLIQEAKAQAQSENEDDVCFIVLNRKEGSGLGFSVAGGTDVEPKSITVHRV
	gi 12861607	
20		3610 3620 3630 3640 3650
	NOV8a	FSQGAASQEGTMNRGDFILLSVNCASLAGLAHGVLKVLHQALHKKDALVV
	NOV8b	FSQGAASQEGTMNRGDFILLSVNCASLAGLAHGVLKVLHQALHKKDALVV
25	gi 15295903	FSQGAASQEGTMNRGDFILLSVNCASLAGLAHGVLKVLHQALHKKDALVV
	gi 2224541	FSQGAASQEGTMNRGDFILLSVNCASLAGLAHGVLKVLHQALHKKDALVV
	gi 12621106	FSQGAASQEGTMNRGDFILLSVNCASLAGLAHGVLKVLHQALHKKDALVV
	gi 12751452	FSQGAASQEGTMNRGDFILLSVNCASLAGLAHGVLKVLHQALHKKDALVV
	gi 12861607	
30		3660 3670 3680 3690 3700
	NOV8a	IKKGMQDFPRPSARQEPPTANGKGLLSRKTIPLEPGIGRVSVAHDALCVEV
	NOV8b	IKKGMQDFPRPSARQEPPTANGKGLLSRKTIPLEPGIGRVSVAHDALCVEV
35	gi 15295903	IKKGMQDFPRPSARQEPPTANGKGLLSRKTIPLEPGIGRVSVAHDALCVEV
	gi 2224541	IKKGMQDFPRPSARQEPPTANGKGLLSRKTIPLEPGIGRVSVAHDALCVEV
	gi 12621106	IKKGMQDFPRPSARQEPPTANGKGLLSRKTIPLEPGIGRVSVAHDALCVEV
	gi 12751452	IKKGMQDFPRPSARQEPPTANGKGLLSRKTIPLEPGIGRVSVAHDALCVEV
	gi 12861607	
40		3710 3720 3730 3740 3750
	NOV8a	LKTSAGLGLSLDGKKSSTVGDGPLVIKRVYKGAAEQAGIJFAGDEILAI
	NOV8b	LKTSAGLGLSLDGKKSSTVGDGPLVIKRVYKGAAEQAGIIIEAGDEILAI
45	gi 15295903	LKTSAGLGLSLDGKKSSTVGDGPLVIKRVYKGAAEQAGIIIEAGDEILAI
	gi 2224541	LKTSAGLGLSLDGKKSSTVGDGPLVIKRVYKGAAEQAGIIIEAGDEILAI
	gi 12621106	LKTSAGLGLSLDGKKSSTVGDGPLVIKRVYKGAAEQAGIIIEAGDEILAI
	gi 12751452	LKTSAGLGLSLDGKKSSTVGDGPLVIKRVYKGAAEQAGIIIEAGDEILAI
	gi 12861607	
50		3760 3770 3780
	NOV8a	NGKPLVGLMHDFAWNIMKSVPCEGPVQLLIRKHRNS
	NOV8b	NGKPLVGLMHDFAWNIMKSVPCEGPVQLLIRKHRNS
55	gi 15295903	NGKPLVGLMHDFAWNIMKSVPCEGPVQLLIRKHRNS
	gi 2224541	NGKPLVGLMHDFAWNIMKSVPCEGPVQLLIRKHRNS
	gi 12621106	NGKPLVGLMHDFAWNIMKSVPCEGPVQLLIRKHRNS
	gi 12751452	NGKPLVGLMHDFAWNIMKSVPCEGPVQLLIRKHRNS
	gi 12861607	

Table 8H-J lists the domain description from DOMAIN analysis results against NOV8. This indicates that the NOV8 sequence has properties similar to those of other proteins known to contain this domain.

Table 8H. Domain Analysis of NOV8

gnl|Smart|smart00228, PDZ, Domain present in PSD-95, Dlg, and ZO-1/2.; Also called DHR (Dlg homologous region) or GLGF (relatively well conserved tetrapeptide in these domains). Some PDZs have been shown to bind C-terminal polypeptides; others appear to bind internal (non-C-terminal) polypeptides. Different PDZs possess different binding specificities. (SEQ ID NO:86)
CD-Length = 86 residues, 95.3% aligned
Score = 69.3 bits (168), Expect = 3e-12

5	Query: 333 RIWKMEELLKESDGLGIQVSGGRGSKRSPHAIVVTQVKKEGAAHRLRDGRSLSGDELLVIN 392 + + + + + + + +	
	Sbjct: 1 EPRLVELEKGGGGLGFSLVGGKDSDGDD--VVVSSVPGSPAAKAG-LKPGDVILEVN 55	
	Query: 393 GHLLVGLSHEEEAVILRSATGMVQLVV 419 + + + +	
	Sbjct: 56 GTSVEGLTHLEAVDLLKEAGGKVTLTV 82	

10

Table 8I. Domain Analysis of NOV8

gnl|Smart|smart00228, PDZ, Domain present in PSD-95, Dlg, and ZO-1/2.; Also called DHR (Dlg homologous region) or GLGF (relatively well conserved tetrapeptide in these domains). Some PDZs have been shown to bind C-terminal polypeptides; others appear to bind internal (non-C-terminal) polypeptides. Different PDZs possess different binding specificities. (SEQ ID NO:86)
CD-Length = 86 residues, 96.5% aligned
Score = 66.2 bits (160), Expect = 2e-11

15	Query: 556 ISIIGLYKEKGKGLGFSIAGGRDCIRGQMGIFVKTIFPNGSAEDGRLKEGDEILDVN 615 ++ + + + ++ + +	
	Sbjct: 2 PRLVELEKGGG-GLGFSLVGGKD--SGDGGVVVSSVPGSPAAKAG-LKPGDVILEVNGT 57	
	Query: 616 PIKGLTFQEAHTFKQIRSGLFVLTVR 642 ++ + + + + +	
	Sbjct: 58 SVEGLTHLEAVDLLKEAGGKVTLTVR 84	

20

Table 8J. Domain Analysis of NOV8

gnl|Smart|smart00228, PDZ, Domain present in PSD-95, Dlg, and ZO-1/2.; Also called DHR (Dlg homologous region) or GLGF (relatively well conserved tetrapeptide in these domains). Some PDZs have been shown to bind C-terminal polypeptides; others appear to bind internal (non-C-terminal) polypeptides. Different PDZs possess different binding specificities. (SEQ ID NO:86)
CD-Length = 86 residues, 97.7% aligned
Score = 60.1 bits (144), Expect = 2e-09

25	Query: 2597 FIVLNRKEGSGLGFSVAGGTDVEPKSITVHRVFSQGAASQEGLMNRGDFLLSVNGASLAG 2656 + + + + + +	
	Sbjct: 3 RLVELEKGGGGLGFSLVGGKDSDGDDGVVSSVPGSPAAKAG-LKPGDVILEVNGTSVEG 61	

Query: 2657 LAHGNVLKVLHQAQLHKDALVVIKKG 2682
| | + + | + | | | | ++ |
Sbjct: 62 LTHLEAVDLLKEAG-GKVTLTVLRGG 86

5

Proteins belonging to the IGFBP-ALS family of proteins play an important role in regulating the levels of circulating hormones. The acid labile subunit of the complex plays an important role in regulating the stability of the complex and ensuring high levels of circulating hormones that are regulated by the IGFBP family of proteins. This protein also has a leucine rich repeat that is a common domain in many proteins that are important for the developing embryo. As a result this protein may play an important role in development and disease.

Insulin-like growth factors (IGFs) I and II are important regulators of cell proliferation and differentiation (Ueki I et al., Proc Natl Acad Sci U S A 2000 Jun 6;97(12):6868-73). After birth, plasma IGFs, representing mostly liver-derived IGFs, circulate in ternary complexes of 150 kDa consisting of one molecule each of IGF, IGF-binding protein (IGFBP) 3, and an acid labile subunit (ALS). Onset of ALS synthesis after birth is the primary factor driving the formation of ternary complexes. Capture of IGFs by ALS is thought to allow the development of a plasma reservoir without negative effects such as hypoglycemia and cell proliferation. To evaluate the importance of ALS and ternary complexes, mice have been created in which the 20 ALS gene has been inactivated. The mutation was inherited in a Mendelian manner, without any effects on survival rates and birth weights. A growth deficit was observed in null mice after 3 weeks of life and reached 13% by 10 weeks. This modest phenotype was observed despite reductions of 62 and 88% in the concentrations of plasma IGF-I and IGFBP-3, respectively. Increased turnover accounted for these reductions because indices of synthesis in 25 liver and kidney were not decreased. Surprisingly, absence of ALS did not affect glucose and insulin homeostasis. Therefore, ALS is required for postnatal accumulation of IGF-I and IGFBP-3 but, consistent with findings supporting a predominant role for locally produced IGF-I, is not critical for growth. This model should be useful to determine whether presence of 30 ALS is needed for other actions of liver-derived IGF-I and for maintenance of homeostasis in presence of high circulating levels of IGF-II.

In the circulation, insulin-like growth factor-I (IGF-I) is bound in a trimeric complex of 150 kDa with IGF binding protein-3 (IGFBP-3) and the acid-labile subunit (ALS). (Moller S et al., J Hepatol 2000 Mar;32(3):441-6). Whereas circulating IGF-I and IGFBP-3 are reported to be low in patients with chronic liver failure, the level of ALS has not been described in 35 relation to hepatic dysfunction. The aim of the present study was therefore to measure

circulating and hepatic venous concentrations of ALS in relation to hepatic function and the IGF axis.

The insulin-like growth factor (IGF) binding proteins (IGFBPs) were initially identified as carrier proteins for IGF-I and IGF-II in a variety of biologic fluids (Rosenfeld RG et al., Pediatrics 1999 Oct;104(4 Pt 2):1018-21). Their presumed function was to protect IGF peptides from degradation and clearance, increase the half-life of the IGFs, and deliver them to appropriate tissue receptors. The concept of IGFBPs as simple carrier proteins has been complicated, however, by a number of observations: 1) the six IGFBPs vary in their tissue expression and their regulation by other hormones and growth factors; 2) the IGFBPs are subjected to proteolytic degradation, thereby altering their affinities for the IGFs; 3) IGFBP-3 and IGFBP-5, in addition to binding IGFs, also can associate with an acid-labile subunit, thereby increasing further the half-life of the IGFs; 4) in addition to modifying the access of IGF peptides to IGF and insulin receptors, several of the IGFBPs may be capable of increasing IGF action; 5) some of the IGFBPs may be capable of IGF-independent regulation of cell growth; 6) some of the IGFBPs are associated with cell membranes or possibly with membrane receptors; and 7) some of the IGFBPs have nuclear recognition sites and may be found within the nucleus. Additionally, a number of cDNAs identified recently have been found to encode proteins that bind IGFs, but with substantially lower affinities than is the case with IGFBPs. The N-terminal regions of the predicted proteins are structurally homologous to the classic IGFBPs, with conservation of the cysteine-rich region. These observations suggest that these low-affinity binders are members of an IGFBP superfamily, capable of regulating cell growth by both IGF-dependent and IGF-independent mechanisms.

Total IGF-I level in serum is a sensitive index during growth hormone (GH) replacement therapy of adults, since GH stimulates the hepatic expressions of both insulin-like growth factor (IGF-I) and acid-labile subunit (ALS) and the major part of IGF-I in the circulation is found in a ternary complex together with ALS and IGFBP-3 (Hall K et al., J Endocrinol Invest 1999;22(5 Suppl):48-57). However, other regulators of the proteins constituting the ternary complex may influence IGF-I levels. In healthy subjects the serum IGF-I levels are low at birth, rise during childhood, with peak levels during puberty, and decline with increasing age. This pattern has been attributed to the age-dependent GH production, but it is unknown whether the wide range of IGF-I levels within each age interval is due to GH production or GH sensitivity. In elderly twins approximately 60% of IGF-I levels are genetically determined. The remaining environmental dependency of IGF-I is partly due to

nutrition. Both caloric and protein content of the diet is of importance. Thus, low IGF-I levels are found in GH deficient patients as well as in patients with GH resistance due to malnutrition or GH receptor defects. It is essential that IGF-I determination is performed by assays in which IGFBPs do not interfere, and that IGF-I concentration is evaluated in relation to age, i.e. 5 expressed in SD score, and the number of individuals constituting the reference intervals improves the sensitivity and specificity. Although determination of IGF-I is recommended in assessing GH deficiency in children, its diagnostic value in patients with adult onset of GH deficiency is not agreed upon. In the age group above 40-80 years many patients with pituitary/hypothalamic disorders and GH peaks below 3 microg/l during provocation tests 10 have normal IGF-I levels. It is not clarified, whether the IGF-I levels within normal range for age is due to endogenous basal GH production being sufficient or other factors stimulating IGF-I, IGFBP-3 or ALS expressions.

Circulating insulin-like growth factors (IGFs) represent an important pool of potential hypoglycemic activity, which is largely inhibited by their sequestration in a heterotrimeric 15 complex comprising growth factor, IGF-binding protein-3 (IGFBP-3), and acid-labile subunit (ALS) (Baxter RC Metabolism 1995 Oct;44(10 Suppl 4):12-7). Less than 1% of total IGFs circulate in the free form, yet even this amount might contribute significantly to circulating insulin-like activity. The ternary binding protein complex appears to inhibit insulin-like activity of bound IGFs by preventing their egress from the circulation. Although the integrity 20 of this complex might be affected by limited proteolysis of IGFBP-3 in pregnancy and catabolic conditions, the evidence that this increases IGF bioavailability, and thus hypoglycemic potential, is as yet unclear. However, in patients with IGF-II-secreting tumors, 25 hypoglycemia may result from a failure of the ternary complex to adequately sequester the IGFs. Improvement in complex formation, by treatment with corticosteroids or growth hormone, alleviates the hypoglycemia, even if (as seen with growth hormone treatment) IGF-II hypersecretion persists. In these patients, blood glucose levels are inversely correlated with IGFBP-2 levels, suggesting that this protein might play a part in transporting IGFs to their target tissues. Conversely, ALS levels correlate positively with blood glucose, emphasizing 30 the importance of the ternary complex in preventing hypoglycemia. Unlike the other IGF-binding proteins, IGFBP-1 is acutely regulated in the circulation, in a manner consistent with its acting as a glucose counterregulator. It might act in this way by inhibiting the activity of free IGFs in the circulation.

Leucine-rich repeats (LRRs) are relatively short motifs (22-28 residues in length) found in a variety of cytoplasmic, membrane and extracellular proteins (InterPro). Although

these proteins are associated with widely different functions, a common property involves protein-protein interaction. Little is known about the 3D structure of LRRs, although it is believed that they can form amphipathic structures with hydrophobic surfaces capable of interacting with membranes. *In vitro* studies of a synthetic LRR from Drosophila Toll protein have indicated that the peptides form gels by adopting beta-sheet structures that form extended filaments. These results are consistent with the idea that LRRs mediate protein-protein interactions and cellular adhesion. Other functions of LRR-containing proteins include, for example, binding to enzymes and vascular repair. The 3-D structure of ribonuclease inhibitor, a protein containing 15 LRRs, has been determined, revealing LRRs to be a new class of alpha/beta fold. LRRs form elongated non-globular structures and are often flanked by cysteine rich domains.

The disclosed NOV8 nucleic acid of the invention encoding a papin-like protein includes the nucleic acid whose sequence is provided in Table 8A and C, or a fragment thereof. The invention also includes a mutant or variant nucleic acid any of whose bases may be changed from the corresponding base shown in Table 8A and C while still encoding a protein that maintains its papin-like activities and physiological functions, or a fragment of such a nucleic acid. The invention further includes nucleic acids whose sequences are complementary to those just described, including nucleic acid fragments that are complementary to any of the nucleic acids just described. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications. Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject. In the mutant or variant nucleic acids, and their complements, up to about 12% percent of the bases may be so changed.

The disclosed NOV8 protein of the invention includes the papin-like protein whose sequence is provided in Table 8B and D. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in Table 2 while still encoding a protein that maintains its papin-like activities and physiological functions, or a functional fragment thereof. In the mutant or variant protein, up to about 43% percent of the residues may be so changed.

The invention further encompasses antibodies and antibody fragments, such as F_{ab} or (F_{ab})₂, that bind immunospecifically to any of the proteins of the invention.

The above defined information for this invention suggests that this papin-like protein (NOV8) may function as a member of a "papin family". Therefore, the NOV8 nucleic acids and proteins identified here may be useful in potential therapeutic applications implicated in (but not limited to) various pathologies and disorders as indicated below. The potential 5 therapeutic applications for this invention include, but are not limited to: protein therapeutic, small molecule drug target, antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), diagnostic and/or prognostic marker, gene therapy (gene delivery/gene ablation), research tools, tissue regeneration *in vivo* and *in vitro* of all tissues and cell types composing (but not limited to) those defined here.

10 The NOV8 nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in cancer including but not limited to Inflammation, Autoimmune disorders, Aging and Cancer. For example, a cDNA encoding the papin-like protein (NOV8) may be useful in gene therapy, and the papin-like protein (NOV8) may be useful when administered to a subject in need thereof. By way of nonlimiting example, the 15 compositions of the present invention will have efficacy for treatment of patients suffering from cancer, cystitis, incontinence, fertility, cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis , atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis , subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, obesity, transplantation 20 recovery. The NOV8 nucleic acid encoding papin-like protein, and the papin-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

NOV8 nucleic acids and polypeptides are further useful in the generation of antibodies 25 that bind immuno-specifically to the novel NOV8 substances for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-NOVX Antibodies" section below. The disclosed NOV8 protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated NOV8 epitope is from about amino acids 10 to 50. In another embodiment, a NOV8 epitope is from about amino 30 acids 80 to 120. In additional embodiments, NOV8 epitopes are from about amino acids 180 to 220, from about amino acids 230 to 300, from about amino acid 330 to 350, from about amino acid 370 to 400, from about amino acid 480 to 540, from about amino acid 550 to 560, and from about amino acids 620 to 840. These novel proteins can be used in assay systems for

functional analysis of various human disorders, which will help in understanding of pathology of the disease and development of new drug targets for various disorders.

NOVX Nucleic Acids and Polypeptides

One aspect of the invention pertains to isolated nucleic acid molecules that encode NOVX polypeptides or biologically active portions thereof. Also included in the invention are nucleic acid fragments sufficient for use as hybridization probes to identify NOVX-encoding nucleic acids (e.g., NOVX mRNAs) and fragments for use as PCR primers for the amplification and/or mutation of NOVX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA), RNA molecules (e.g., mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule may be single-stranded or double-stranded, but preferably is comprised double-stranded DNA.

An NOVX nucleic acid can encode a mature NOVX polypeptide. As used herein, a "mature" form of a polypeptide or protein disclosed in the present invention is the product of a naturally occurring polypeptide or precursor form or proprotein. The naturally occurring polypeptide, precursor or proprotein includes, by way of nonlimiting example, the full-length gene product, encoded by the corresponding gene. Alternatively, it may be defined as the polypeptide, precursor or proprotein encoded by an ORF described herein. The product "mature" form arises, again by way of nonlimiting example, as a result of one or more naturally occurring processing steps as they may take place within the cell, or host cell, in which the gene product arises. Examples of such processing steps leading to a "mature" form of a polypeptide or protein include the cleavage of the N-terminal methionine residue encoded by the initiation codon of an ORF, or the proteolytic cleavage of a signal peptide or leader sequence. Thus a mature form arising from a precursor polypeptide or protein that has residues 1 to N, where residue 1 is the N-terminal methionine, would have residues 2 through N remaining after removal of the N-terminal methionine. Alternatively, a mature form arising from a precursor polypeptide or protein having residues 1 to N, in which an N-terminal signal sequence from residue 1 to residue M is cleaved, would have the residues from residue M+1 to residue N remaining. Further as used herein, a "mature" form of a polypeptide or protein may arise from a step of post-translational modification other than a proteolytic cleavage event. Such additional processes include, by way of non-limiting example, glycosylation,

myristylation or phosphorylation. In general, a mature polypeptide or protein may result from the operation of only one of these processes, or a combination of any of them.

The term "probes", as utilized herein, refers to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as 5 approximately, e.g., 6,000 nt, depending upon the specific use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are generally obtained from a natural or recombinant source, are highly specific, and much slower to hybridize than shorter-length oligomer probes. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization 10 technologies, or ELISA-like technologies.

The term "isolated" nucleic acid molecule, as utilized herein, is one, which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5'- and 3'-termini of the nucleic acid) in the genomic DNA 15 of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated NOVX nucleic acid molecules can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell/tissue from which the nucleic acid is derived (*e.g.*, brain, heart, liver, spleen, etc.). Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can 20 be substantially free of other cellular material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, or a 25 complement of this aforementioned nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26 as a hybridization probe, NOVX molecules can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook, *et al.*, (eds.), 30 MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard

PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to NOVX nucleotide sequences can be prepared by standard synthetic techniques, e.g., using an automated DNA synthesizer.

- 5 As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue.
- 10 Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment of the invention, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, or a complement thereof. Oligonucleotides may be chemically synthesized and may also be used as probes.
- 15

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, or a portion of this nucleotide sequence (e.g., a fragment that can be used as a probe or primer or a fragment encoding a biologically-active portion of an NOVX polypeptide). A nucleic acid molecule that is complementary to the nucleotide sequence shown SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, or 26 is one that is sufficiently complementary to the nucleotide sequence shown SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, or 26 that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, thereby forming a stable duplex.

20 As used herein, the term "complementary" refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term "binding" means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, van der Waals, hydrophobic interactions, and the like. A physical interaction can be either direct or indirect. Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively, and are at most some portion less than a full length sequence.

- 5 Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type. Homologs are nucleic acid sequences or amino acid sequences of a particular gene that are derived from different species.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or 15 analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the invention, in various embodiments, by at least about 70%, 80%, or 95% identity (with a preferred identity of 80-95%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a 20 computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. *See e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below.

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or 25 variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of NOVX polypeptides. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the invention, homologous 30 nucleotide sequences include nucleotide sequences encoding for an NOVX polypeptide of species other than humans, including, but not limited to: vertebrates, and thus can include, *e.g.*, frog, mouse, rat, rabbit, dog, cat cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence

does not, however, include the exact nucleotide sequence encoding human NOVX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, as well as a polypeptide possessing NOVX biological activity. Various 5 biological activities of the NOVX proteins are described below.

An NOVX polypeptide is encoded by the open reading frame ("ORF") of an NOVX nucleic acid. An ORF corresponds to a nucleotide sequence that could potentially be translated into a polypeptide. A stretch of nucleic acids comprising an ORF is uninterrupted by a stop codon. An ORF that represents the coding sequence for a full protein begins with an ATG 10 "start" codon and terminates with one of the three "stop" codons, namely, TAA, TAG, or TGA. For the purposes of this invention, an ORF may be any part of a coding sequence, with or without a start codon, a stop codon, or both. For an ORF to be considered as a good candidate for coding for a *bona fide* cellular protein, a minimum size requirement is often set, e.g., a stretch of DNA that would encode a protein of 50 amino acids or more.

15 The nucleotide sequences determined from the cloning of the human NOVX genes allows for the generation of probes and primers designed for use in identifying and/or cloning NOVX homologues in other cell types, e.g. from other tissues, as well as NOVX homologues from other vertebrates. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that 20 hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 consecutive sense strand nucleotide sequence SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, or 26; or an anti-sense strand nucleotide sequence of SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, or 26; or of a naturally occurring mutant of SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26.

25 Probes based on the human NOVX nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, e.g. the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissues which mis-express an NOVX protein, such as by measuring a level of an NOVX-encoding nucleic acid in 30 a sample of cells from a subject e.g., detecting NOVX mRNA levels or determining whether a genomic NOVX gene has been mutated or deleted.

"A polypeptide having a biologically-active portion of an NOVX polypeptide" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a

polypeptide of the invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically-active portion of NOVX" can be prepared by isolating a portion SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, or 26, that encodes a polypeptide having an NOVX biological activity (the biological activities of the NOVX proteins are described below), expressing the encoded portion of NOVX protein (e.g., by recombinant expression *in vitro*) and assessing the activity of the encoded portion of NOVX.

NOVX Nucleic Acid and Polypeptide Variants

The invention further encompasses nucleic acid molecules that differ from the 10 nucleotide sequences shown in SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26 due to degeneracy of the genetic code and thus encode the same NOVX proteins as that encoded by the nucleotide sequences shown in SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in SEQ 15 ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27.

In addition to the human NOVX nucleotide sequences shown in SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of the NOVX polypeptides may exist within a population (e.g., the human population). Such genetic 20 polymorphism in the NOVX genes may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame (ORF) encoding an NOVX protein, preferably a vertebrate NOVX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the NOVX genes. Any and all such nucleotide 25 variations and resulting amino acid polymorphisms in the NOVX polypeptides, which are the result of natural allelic variation and that do not alter the functional activity of the NOVX polypeptides, are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding NOVX proteins from other species, and thus that have a nucleotide sequence that differs from the human SEQ ID NOS:1, 3, 4, 6, 8, 30 10, 12, 14, 16, 18, 20, 22, 24, and 26 are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the NOVX cDNAs of the invention can be isolated based on their homology to the human NOVX nucleic

acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the 5 nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26. In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500, 750, 1000, 1500, or 2000 or more nucleotides in length. In yet another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to 10 describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding NOVX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe 15 using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5 °C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at T_m, 20 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at 25 pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (*e.g.*, 10 nt to 50 nt) and at least about 60°C for longer probes, primers and 30 oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%,

70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions are hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C, followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequences SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well-known within the art. See, e.g., Ausubel, et al. (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990; GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequences SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (e.g., as employed for cross-species hybridizations). See, e.g., Ausubel, et al. (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981. *Proc Natl Acad Sci USA* 78: 6789-6792.

Conservative Mutations

In addition to naturally-occurring allelic variants of NOVX sequences that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequences SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 5 24, and 26, thereby leading to changes in the amino acid sequences of the encoded NOVX proteins, without altering the functional ability of said NOVX proteins. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27. A "non-essential" amino acid residue is a residue that can be altered from the wild-type 10 sequences of the NOVX proteins without altering their biological activity, whereas an "essential" amino acid residue is required for such biological activity. For example, amino acid residues that are conserved among the NOVX proteins of the invention are predicted to be particularly non-amenable to alteration. Amino acids for which conservative substitutions can be made are well-known within the art.

15 Another aspect of the invention pertains to nucleic acid molecules encoding NOVX proteins that contain changes in amino acid residues that are not essential for activity. Such NOVX proteins differ in amino acid sequence from SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26 yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein 20 comprises an amino acid sequence at least about 45% homologous to the amino acid sequences SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25; and 27. Preferably, the protein encoded by the nucleic acid molecule is at least about 60% homologous to SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 27; more preferably at least about 70% homologous SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27; still more preferably 25 at least about 80% homologous to SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27; even more preferably at least about 90% homologous to SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27; and most preferably at least about 95% homologous to SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27.

An isolated nucleic acid molecule encoding an NOVX protein homologous to the 30 protein of SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27 can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26 by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted, non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined within the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted non-essential amino acid residue in the NOVX protein is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an NOVX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for NOVX biological activity to identify mutants that retain activity. Following mutagenesis SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

The relatedness of amino acid families may also be determined based on side chain interactions. Substituted amino acids may be fully conserved "strong" residues or fully conserved "weak" residues. The "strong" group of conserved amino acid residues may be any one of the following groups: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW, wherein the single letter amino acid codes are grouped by those amino acids that may be substituted for each other. Likewise, the "weak" group of conserved residues may be any one of the following: CSA, ATV, SAG, STNK, STPA, SGND, SNDEQK, NDEQHK, NEQHRK, VLIM, HFY, wherein the letters within each group represent the single letter amino acid code.

In one embodiment, a mutant NOVX protein can be assayed for (i) the ability to form protein:protein interactions with other NOVX proteins, other cell-surface proteins, or biologically-active portions thereof, (ii) complex formation between a mutant NOVX protein and an NOVX ligand; or (iii) the ability of a mutant NOVX protein to bind to an intracellular target protein or biologically-active portion thereof; (e.g. avidin proteins).

In yet another embodiment, a mutant NOVX protein can be assayed for the ability to regulate a specific biological function (e.g., regulation of insulin release).

Antisense Nucleic Acids

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, or 5 fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein (e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence). In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides 10 or an entire NOVX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of an NOVX protein of SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27, or antisense nucleic acids complementary to an NOVX nucleic acid sequence of SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, are additionally provided.

15 In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an NOVX protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence 20 encoding the NOVX protein. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding the NOVX protein disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and 25 Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of NOVX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of NOVX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of NOVX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 30 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally-occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the

physical stability of the duplex formed between the antisense and sense nucleic acids (e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used).

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, 5 xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, 10 beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the 15 antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a 20 subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an NOVX protein to thereby inhibit expression of the protein (e.g., by inhibiting transcription and/or translation). The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an 25 antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered 30 systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface (e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens). The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient nucleic acid molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other. *See, e.g., Gaultier, et al., 1987. Nucl. Acids Res. 15: 6625-6641.*

- 5 The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (*See, e.g., Inoue, et al. 1987. Nucl. Acids Res. 15: 6131-6148*) or a chimeric RNA-DNA analogue (*See, e.g., Inoue, et al., 1987. FEBS Lett. 215: 327-330.*

Ribozymes and PNA Moieties

10 Nucleic acid modifications include, by way of non-limiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

15 In one embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g., hammerhead ribozymes as described in Haselhoff and Gerlach 1988. Nature 334: 585-591*) can be used to catalytically cleave NOVX mRNA transcripts to thereby inhibit translation of NOVX mRNA. A ribozyme having specificity for an NOVX-encoding nucleic acid can be designed based upon the nucleotide sequence of an NOVX cDNA disclosed herein (*i.e., SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26*). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an NOVX-encoding mRNA. *See, e.g., U.S. Patent 4,987,071 to Cech, et al. and U.S. Patent 5,116,742 to Cech, et al.* NOVX mRNA can also be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. *See, e.g., Bartel et al., (1993) Science 261:1411-1418.*

30 Alternatively, NOVX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the NOVX nucleic acid (*e.g., the NOVX promoter and/or enhancers*) to form triple helical structures that prevent transcription of the NOVX gene in target cells. *See, e.g., Helene, 1991. Anticancer Drug Des. 6: 569-84; Helene, et al. 1992. Ann. N.Y. Acad. Sci. 660: 27-36; Maher, 1992. Bioassays 14: 807-15.*

In various embodiments, the NOVX nucleic acids can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids. See, e.g., Hyrup, et al., 1996. *Bioorg Med Chem* 4: 5-23. As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics (e.g., DNA mimics) in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup, et al., 1996. *supra*; Perry-O'Keefe, et al., 1996. *Proc. Natl. Acad. Sci. USA* 93: 14670-14675.

PNAs of NOVX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of NOVX can also be used, for example, in the analysis of single base pair mutations in a gene (e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S₁ nucleases (See, Hyrup, et al., 1996. *supra*); or as probes or primers for DNA sequence and hybridization (See, Hyrup, et al., 1996, *supra*; Perry-O'Keefe, et al., 1996. *supra*).

In another embodiment, PNAs of NOVX can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of NOVX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes (e.g., RNase H and DNA polymerases) to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (see, Hyrup, et al., 1996. *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup, et al., 1996. *supra* and Finn, et al., 1996. *Nucl Acids Res* 24: 3357-3363. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, e.g., 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA. See, e.g., Mag, et al., 1989. *Nucl Acid Res* 17: 5973-5988. PNA monomers are then coupled in a stepwise manner

to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment. *See, e.g.*, Finn, *et al.*, 1996. *supra*. Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. *See, e.g.*, Petersen, *et al.*, 1975. *Bioorg. Med. Chem. Lett.* 5: 1119-1124.

5 In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (*see, e.g.*, Letsinger, *et al.*, 1989. *Proc. Natl. Acad. Sci. U.S.A.* 86: 6553-6556; Lemaitre, *et al.*, 1987. *Proc. Natl. Acad. Sci.* 84: 648-652; PCT Publication No. WO88/09810) or the blood-brain barrier (*see, e.g.*, PCT Publication No. WO 89/10134). In 10 addition, oligonucleotides can be modified with hybridization triggered cleavage agents (*see, e.g.*, Krol, *et al.*, 1988. *BioTechniques* 6:958-976) or intercalating agents (*see, e.g.*, Zon, 1988. *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, and the like.

15 **NOVX Polypeptides**

A polypeptide according to the invention includes a polypeptide including the amino acid sequence of NOVX polypeptides whose sequences are provided in SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residues shown in SEQ ID 20 NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27 while still encoding a protein that maintains its NOVX activities and physiological functions, or a functional fragment thereof.

In general, an NOVX variant that preserves NOVX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between 25 two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above.

One aspect of the invention pertains to isolated NOVX proteins, and biologically- 30 active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-NOVX antibodies. In one embodiment, native NOVX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another

embodiment, NOVX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, an NOVX protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" polypeptide or protein or biologically-active portion thereof
5 is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the NOVX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of NOVX proteins in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly-produced. In
10 one embodiment, the language "substantially free of cellular material" includes preparations of NOVX proteins having less than about 30% (by dry weight) of non-NOVX proteins (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-NOVX proteins, still more preferably less than about 10% of non-NOVX proteins, and most preferably less than about 5% of non-NOVX proteins. When the NOVX protein or
15 biologically-active portion thereof is recombinantly-produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the NOVX protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes
20 preparations of NOVX proteins in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of NOVX proteins having less than about 30% (by dry weight) of chemical precursors or non-NOVX chemicals, more preferably less than about 20% chemical precursors or
25 non-NOVX chemicals, still more preferably less than about 10% chemical precursors or non-NOVX chemicals, and most preferably less than about 5% chemical precursors or non-NOVX chemicals.

Biologically-active portions of NOVX proteins include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequences of the
30 NOVX proteins (*e.g.*, the amino acid sequence shown in SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27) that include fewer amino acids than the full-length NOVX proteins, and exhibit at least one activity of an NOVX protein. Typically, biologically-active portions comprise a domain or motif with at least one activity of the NOVX protein. A biologically-

active portion of an NOVX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acid residues in length.

Moreover, other biologically-active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native NOVX protein.

In an embodiment, the NOVX protein has an amino acid sequence shown SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27. In other embodiments, the NOVX protein is substantially homologous to SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27, and retains the functional activity of the protein of SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27, yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail, below. Accordingly, in another embodiment, the NOVX protein is a protein that comprises an amino acid sequence at least about 45% homologous to the amino acid sequence SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27, and retains the functional activity of the NOVX proteins of SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27.

Determining Homology Between Two or More Sequences

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. See, Needleman and Wunsch, 1970. *J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or

99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26.

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region.

Chimeric and Fusion Proteins

The invention also provides NOVX chimeric or fusion proteins. As used herein, an NOVX "chimeric protein" or "fusion protein" comprises an NOVX polypeptide operatively-linked to a non-NOVX polypeptide. An "NOVX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an NOVX protein SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, or 27, whereas a "non-NOVX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the NOVX protein, *e.g.*, a protein that is different from the NOVX protein and that is derived from the same or a different organism. Within an NOVX fusion protein the NOVX polypeptide can correspond to all or a portion of an NOVX protein. In one embodiment, an NOVX fusion protein comprises at least one biologically-active portion of an NOVX protein. In another embodiment, an NOVX fusion protein comprises at least two biologically-active portions of an NOVX protein. In yet another embodiment, an NOVX fusion protein comprises at least three biologically-active portions of an NOVX protein. Within the fusion protein, the term "operatively-linked" is intended to indicate that the NOVX polypeptide and the non-NOVX polypeptide are fused in-frame with one another. The non-NOVX polypeptide can be fused to the N-terminus or C-terminus of the NOVX polypeptide.

In one embodiment, the fusion protein is a GST-NOVX fusion protein in which the NOVX sequences are fused to the C-terminus of the GST (glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant NOVX polypeptides.

5 In another embodiment, the fusion protein is an NOVX protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of NOVX can be increased through use of a heterologous signal sequence.

In yet another embodiment, the fusion protein is an NOVX-immunoglobulin fusion 10 protein in which the NOVX sequences are fused to sequences derived from a member of the immunoglobulin protein family. The NOVX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between an NOVX ligand and an NOVX protein on the surface of a cell, to thereby suppress NOVX-mediated signal transduction *in vivo*. The NOVX-immunoglobulin 15 fusion proteins can be used to affect the bioavailability of an NOVX cognate ligand.

Inhibition of the NOVX ligand/NOVX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (*e.g.* promoting or inhibiting) cell survival. Moreover, the NOVX-immunoglobulin fusion proteins of the 20 invention can be used as immunogens to produce anti-NOVX antibodies in a subject, to purify NOVX ligands, and in screening assays to identify molecules that inhibit the interaction of NOVX with an NOVX ligand.

An NOVX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different 25 polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be 30 carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (*see, e.g.*, Ausubel, *et al.* (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An NOVX-encoding

nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the NOVX protein.

NOVX Agonists and Antagonists

5 The invention also pertains to variants of the NOVX proteins that function as either NOVX agonists (*i.e.*, mimetics) or as NOVX antagonists. Variants of the NOVX protein can be generated by mutagenesis (*e.g.*, discrete point mutation or truncation of the NOVX protein). An agonist of the NOVX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the NOVX protein. An antagonist of 10 the NOVX protein can inhibit one or more of the activities of the naturally occurring form of the NOVX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the NOVX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities 15 of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the NOVX proteins.

Variants of the NOVX proteins that function as either NOVX agonists (*i.e.*, mimetics) or as NOVX antagonists can be identified by screening combinatorial libraries of mutants (*e.g.*, truncation mutants) of the NOVX proteins for NOVX protein agonist or antagonist 20 activity. In one embodiment, a variegated library of NOVX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of NOVX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential NOVX sequences is expressible as individual polypeptides, or 25 alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of NOVX sequences therein. There are a variety of methods which can be used to produce libraries of potential NOVX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate 30 set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential NOVX sequences. Methods for synthesizing degenerate oligonucleotides are well-known within the art. *See, e.g.*, Narang, 1983. *Tetrahedron* 39: 3; Itakura, *et al.*, 1984. *Annu. Rev. Biochem.* 53: 323; Itakura, *et al.*, 1984. *Science* 198: 1056; Ike, *et al.*, 1983. *Nucl. Acids Res.* 11: 477.

Polypeptide Libraries

In addition, libraries of fragments of the NOVX protein coding sequences can be used to generate a variegated population of NOVX fragments for screening and subsequent selection of variants of an NOVX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an NOVX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double-stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S₁ nuclease, and ligating the resulting fragment library into an expression vector. By this method, expression libraries can be derived which encodes N-terminal and internal fragments of various sizes of the NOVX proteins.

Various techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of NOVX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify NOVX variants.

See, e.g., Arkin and Yourvan, 1992. *Proc. Natl. Acad. Sci. USA* 89: 7811-7815; Delgrave, et al., 1993. *Protein Engineering* 6:327-331.

Anti-NOVX Antibodies

Also included in the invention are antibodies to NOVX proteins, or fragments of NOVX proteins. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab}, F_{ab'} and F_{(ab)2} fragments, and an F_{ab} expression library. In general, an antibody molecule

obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated NOVX-related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of NOVX-related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human NOVX-related protein sequence will indicate which regions of a NOVX-related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow and Lane, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native 10 protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of 15 such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, 20 peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be 25 isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity 30 chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, MONOCLONAL ANTIBODIES: PRINCIPLES AND PRACTICE, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the

production of human monoclonal antibodies (Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur et al., MONOCLONAL ANTIBODY PRODUCTION TECHNIQUES AND APPLICATIONS, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for
5 the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by
10 the Scatchard analysis of Munson and Pollard, *Anal. Biochem.*, 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this
15 purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel
20 electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the
25 heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also
30 can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, *Nature* 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant

domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

Humanized Antibodies

5 The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeyen et al., *Science*, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the 10 corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically 15 two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, *Curr. Op. 20 Struct. Biol.*, 2:593-596 (1992)).

Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. 30 Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: *MONOCLONAL ANTIBODIES AND CANCER THERAPY*, Alan R. Liss, Inc., pp. 77-96). Human monoclonal

antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

5 In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon
10 challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (*Bio/Technology* 10, 779-783 (1992)); Lonberg et al. (*Nature* 368 856-859 (1994)); Morrison (*Nature* 368, 812-13 (1994)); Fishwild
15 et al., (*Nature Biotechnology* 14, 845-51 (1996)); Neuberger (*Nature Biotechnology* 14, 826 (1996)); and Lonberg and Huszar (*Intern. Rev. Immunol.* 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication
20 WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as
25 progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an
30 immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be

further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab)2} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab)2} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the 5 binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different 10 specificities (Milstein and Cuello, *Nature*, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 15 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part 20 of the hinge, CH₂, and CH₃ regions. It is preferred to have the first heavy-chain constant region (CH₁) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair 25 of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH₃ region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side 30 chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., *Science* 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., *J. Exp. Med.* 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., *J. Immunol.* 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., *J. Immunol.* 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc γ R), such as Fc γ RI (CD64), Fc γ RII (CD32) and Fc γ RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

15 **Heteroconjugate Antibodies**

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptopbutyrimidate and those disclosed, for example, in U.S. Patent No. 25 4,676,980.

Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., *J. Exp Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with

enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., *Anti-Cancer Drug Design*, 3: 219-230 (1989).

5

Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the trichothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ²¹²Bi, ¹³¹I, ¹³¹In, ⁹⁰Y, and ¹⁸⁶Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., *Science*, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation

using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of an NOVX protein is facilitated by generation of hybridomas that bind to the fragment of an NOVX protein possessing such a domain. Thus, antibodies that are specific for a desired domain within an NOVX protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-NOVX antibodies may be used in methods known within the art relating to the localization and/or quantitation of an NOVX protein (e.g., for use in measuring levels of the NOVX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for NOVX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds (hereinafter "Therapeutics").

An anti-NOVX antibody (e.g., monoclonal antibody) can be used to isolate an NOVX polypeptide by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-NOVX antibody can facilitate the purification of natural NOVX polypeptide from cells and of recombinantly-produced NOVX polypeptide expressed in host cells. Moreover, an anti-NOVX antibody can be used to detect NOVX protein (e.g., in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the NOVX protein. Anti-NOVX antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include

luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

NOVX Recombinant Expression Vectors and Host Cells

5 Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an NOVX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous 10 replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon 15 introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively-linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the 20 plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that 25 the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively-linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably-linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory 30 sequence(s) in a manner that allows for expression of the nucleotide sequence (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell).

The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, GENB EXPRESSION TECHNOLOGY: METHODS IN

ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the 5 design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., NOVX proteins, mutant forms of NOVX proteins, fusion proteins, etc.).

10 The recombinant expression vectors of the invention can be designed for expression of NOVX proteins in prokaryotic or eukaryotic cells. For example, NOVX proteins can be expressed in bacterial cells such as *Escherichia coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San 15 Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *Escherichia coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded 20 therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (i) to increase expression of recombinant protein; (ii) to increase the solubility of the recombinant protein; and (iii) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the 25 recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988. *Gene* 67: 31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse 30 glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION

TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, e.g., Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (see, e.g., Wada, et al., 1992. *Nucl. Acids Res.* 20: 2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the NOVX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *Saccharomyces cerevisiae* include pYEpSec1 (Baldari, et al., 1987. *EMBO J.* 6: 229-234), pMFa (Kurjan and Herskowitz, 1982. *Cell* 30: 933-943), pJRY88 (Schultz et al., 1987. *Gene* 54: 113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (InVitrogen Corp, San Diego, Calif.).

Alternatively, NOVX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., SF9 cells) include the pAc series (Smith, et al., 1983. *Mol. Cell. Biol.* 3: 2156-2165) and the pVL series (Lucklow and Summers, 1989. *Virology* 170: 31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987. *Nature* 329: 840) and pMT2PC (Kaufman, et al., 1987. *EMBO J.* 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, adenovirus 2, cytomegalovirus, and simian virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see, e.g., Chapters 16 and 17 of Sambrook, et al., MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert, et al., 1987. *Genes Dev.* 1: 268-277), lymphoid-specific promoters (Calame and Eaton, 1988. *Adv. Immunol.* 43:

235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989. *EMBO J.* 8: 729-733) and immunoglobulins (Banerji, *et al.*, 1983. *Cell* 33: 729-740; Queen and Baltimore, 1983. *Cell* 33: 741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle, 1989. *Proc. Natl. Acad. Sci. USA* 86: 5473-5477),

5 pancreas-specific promoters (Edlund, *et al.*, 1985. *Science* 230: 912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss, 1990. *Science* 249: 374-379) and the α -fetoprotein promoter (Campes and Tilghman, 1989. *Genes Dev.* 3: 537-546).

10 The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively-linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to NOVX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the
15 antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the
20 control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes *see, e.g.*, Weintraub, *et al.*, "Antisense RNA as a molecular tool for genetic analysis," *Reviews-Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant
25 expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent
30 cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, NOVX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding NOVX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) NOVX protein. Accordingly, the invention further provides methods for producing NOVX protein using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding NOVX protein has been introduced) in a suitable medium such that NOVX protein is produced. In another embodiment, the method further comprises isolating NOVX protein from the medium or the host cell.

Transgenic NOVX Animals

The host cells of the invention can also be used to produce non-human transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which NOVX protein-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous NOVX sequences have been introduced into their genome or homologous recombinant animals in which endogenous NOVX sequences have been altered. Such animals are useful

for studying the function and/or activity of NOVX protein and for identifying and/or evaluating modulators of NOVX protein activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of
5 transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a
10 non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous NOVX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, e.g., an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing NOVX-encoding
15 nucleic acid into the male pronuclei of a fertilized oocyte (e.g., by microinjection, retroviral infection) and allowing the oocyte to develop in a pseudopregnant female foster animal. The human NOVX cDNA sequences SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26 can be introduced as a transgene into the genome of a non-human animal. Alternatively, a non-human homologue of the human NOVX gene, such as a mouse NOVX gene, can be
20 isolated based on hybridization to the human NOVX cDNA (described further *supra*) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably-linked to the NOVX transgene to direct expression of NOVX protein to particular cells. Methods for generating transgenic animals via embryo
25 manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan, 1986. In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based
30 upon the presence of the NOVX transgene in its genome and/or expression of NOVX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene-encoding NOVX protein can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of an NOVX gene into which a deletion, addition or substitution has been introduced to thereby alter, e.g., functionally disrupt, the NOVX gene. The NOVX gene can be a human gene (e.g., the cDNA of SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 5 and 26), but more preferably, is a non-human homologue of a human NOVX gene. For example, a mouse homologue of human NOVX gene of SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26 can be used to construct a homologous recombination vector suitable for altering an endogenous NOVX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous NOVX 10 gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous NOVX gene is mutated or otherwise altered but still encodes functional protein (e.g., the upstream regulatory region can be altered to thereby alter the expression of 15 the endogenous NOVX protein). In the homologous recombination vector, the altered portion of the NOVX gene is flanked at its 5'- and 3'-termini by additional nucleic acid of the NOVX gene to allow for homologous recombination to occur between the exogenous NOVX gene carried by the vector and an endogenous NOVX gene in an embryonic stem cell. The additional flanking NOVX nucleic acid is of sufficient length for successful homologous 20 recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5'- and 3'-termini) are included in the vector. See, e.g., Thomas, *et al.*, 1987. *Cell* 51: 503 for a description of homologous recombination vectors. The vector is then introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced NOVX 25 gene has homologously-recombined with the endogenous NOVX gene are selected. See, e.g., Li, *et al.*, 1992. *Cell* 69: 915.

The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras. See, e.g., Bradley, 1987. In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal 30 and the embryo brought to term. Progeny harboring the homologously-recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously-recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are

described further in Bradley, 1991. *Curr. Opin. Biotechnol.* 2: 823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, See, e.g., Lakso, et al., 1992. *Proc. Natl. Acad. Sci. USA* 89: 6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae*. See, O'Gorman, et al., 1991. *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut, et al., 1997. *Nature* 385: 810-813. In brief, a cell (e.g., a somatic cell) from the transgenic animal can be isolated and induced to exit the growth cycle and enter G₀ phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyst and then transferred to pseudopregnant female foster animal. The offspring borne of this female foster animal will be a clone of the animal from which the cell (e.g., the somatic cell) is isolated.

Pharmaceutical Compositions

The NOVX nucleic acid molecules, NOVX proteins, and anti-NOVX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents

include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, e.g., intravenous, intradermal, subcutaneous, oral (e.g., inhalation), transdermal (*i.e.*, topical), 10 transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such 15 as ethylenediaminetetraacetic acid (EDTA); buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

20 Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be 25 sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. 30 The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents,

for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

5 Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, an NOVX protein or anti-NOVX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from
10 those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be
15 enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or
20 adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a
25 sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

30 Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays

or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (*see, e.g.*, U.S. Patent No. 5,328,470) or by stereotactic injection (*see, e.g.*, Chen, *et al.*, 1994. *Proc. Natl. Acad. Sci. USA* 91: 3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Screening and Detection Methods

The isolated nucleic acid molecules of the invention can be used to express NOVX protein (e.g., via a recombinant expression vector in a host cell in gene therapy applications), to detect NOVX mRNA (e.g., in a biological sample) or a genetic lesion in an NOVX gene, and to modulate NOVX activity, as described further, below. In addition, the NOVX proteins can be used to screen drugs or compounds that modulate the NOVX protein activity or expression as well as to treat disorders characterized by insufficient or excessive production of NOVX protein or production of NOVX protein forms that have decreased or aberrant activity compared to NOVX wild-type protein (e.g.; diabetes (regulates insulin release); obesity (binds and transport lipids); metabolic disturbances associated with obesity, the metabolic syndrome X as well as anorexia and wasting disorders associated with chronic diseases and various cancers, and infectious disease (possesses anti-microbial activity) and the various dyslipidemias. In addition, the anti-NOVX antibodies of the invention can be used to detect and isolate NOVX proteins and modulate NOVX activity. In yet a further aspect, the invention can be used in methods to influence appetite, absorption of nutrients and the disposition of metabolic substrates in both a positive and negative fashion.

The invention further pertains to novel agents identified by the screening assays described herein and uses thereof for treatments as described, *supra*.

Screening Assays

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (e.g., peptides, 25 peptidomimetics, small molecules or other drugs) that bind to NOVX proteins or have a stimulatory or inhibitory effect on, *e.g.*, NOVX protein expression or NOVX protein activity. The invention also includes compounds identified in the screening assays described herein.

In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of the membrane-bound form of an NOVX 30 protein or polypeptide or biologically-active portion thereof. The test compounds of the invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the

"one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds. See, e.g., Lam, 1997. *Anticancer Drug Design* 12: 145.

5 A "small molecule" as used herein, is meant to refer to a composition that has a molecular weight of less than about 5 kD and most preferably less than about 4 kD. Small molecules can be, e.g., nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic or inorganic molecules. Libraries of chemical and/or biological mixtures, such as fungal, bacterial, or algal extracts, are known in the art and can be screened
10 with any of the assays of the invention.

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt, et al., 1993. *Proc. Natl. Acad. Sci. U.S.A.* 90: 6909; Erb, et al., 1994. *Proc. Natl. Acad. Sci. U.S.A.* 91: 11422; Zuckermann, et al., 1994. *J. Med. Chem.* 37: 2678; Cho, et al., 1993. *Science* 261: 1303; Carell, et al., 1994. *Angew. Chem. Int. Ed. Engl.* 33:
15 2059; Carell, et al., 1994. *Angew. Chem. Int. Ed. Engl.* 33: 2061; and Gallop, et al., 1994. *J. Med. Chem.* 37: 1233.

Libraries of compounds may be presented in solution (e.g., Houghten, 1992. *Biotechniques* 13: 412-421), or on beads (Lam, 1991. *Nature* 354: 82-84), on chips (Fodor, 1993. *Nature* 364: 555-556), bacteria (Ladner, U.S. Patent No. 5,223,409), spores (Ladner,
20 U.S. Patent 5,233,409), plasmids (Cull, et al., 1992. *Proc. Natl. Acad. Sci. USA* 89: 1865-1869) or on phage (Scott and Smith, 1990. *Science* 249: 386-390; Devlin, 1990. *Science* 249: 404-406; Cwirla, et al., 1990. *Proc. Natl. Acad. Sci. U.S.A.* 87: 6378-6382; Felici, 1991. *J. Mol. Biol.* 222: 301-310; Ladner, U.S. Patent No. 5,233,409.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a
25 membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to an NOVX protein determined. The cell, for example, can of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the NOVX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic
30 label such that binding of the test compound to the NOVX protein or biologically-active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically-labeled with, for example, horseradish

peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the cell surface with a known compound which

5 binds NOVX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an NOVX protein, wherein determining the ability of the test compound to interact with an NOVX protein comprises determining the ability of the test compound to preferentially bind to NOVX protein or a biologically-active portion thereof as compared to the known compound.

10 In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the NOVX protein or biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of

15 NOVX or a biologically-active portion thereof can be accomplished, for example, by determining the ability of the NOVX protein to bind to or interact with an NOVX target molecule. As used herein, a "target molecule" is a molecule with which an NOVX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses an NOVX interacting protein, a molecule on the surface of a second cell, a molecule in the

20 extracellular milieu, a molecule associated with the internal surface of a cell membrane or a cytoplasmic molecule. An NOVX target molecule can be a non-NOVX molecule or an NOVX protein or polypeptide of the invention. In one embodiment, an NOVX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.* a signal generated by binding of a compound to a membrane-bound

25 NOVX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with NOVX.

Determining the ability of the NOVX protein to bind to or interact with an NOVX target molecule can be accomplished by one of the methods described above for determining

30 direct binding. In one embodiment, determining the ability of the NOVX protein to bind to or interact with an NOVX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+} , diacylglycerol, IP_3 , etc.), detecting catalytic/enzymatic activity of the target an appropriate

substrate, detecting the induction of a reporter gene (comprising an NOVX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, e.g., luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

5 In yet another embodiment, an assay of the invention is a cell-free assay comprising contacting an NOVX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to bind to the NOVX protein or biologically-active portion thereof. Binding of the test compound to the NOVX protein can be determined either directly or indirectly as described above. In one such embodiment, the assay comprises
10 contacting the NOVX protein or biologically-active portion thereof with a known compound which binds NOVX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an NOVX protein, wherein determining the ability of the test compound to interact with an NOVX protein comprises determining the ability of the test compound to preferentially bind to NOVX or biologically-active portion thereof as compared to the known compound.
15

In still another embodiment, an assay is a cell-free assay comprising contacting NOVX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to modulate (e.g. stimulate or inhibit) the activity of the NOVX protein or biologically-active portion thereof. Determining the ability of the test compound to
20 modulate the activity of NOVX can be accomplished, for example, by determining the ability of the NOVX protein to bind to an NOVX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of NOVX protein can be accomplished by determining the ability of the NOVX protein further modulate an NOVX target molecule. For
25 example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as described, *supra*.

In yet another embodiment, the cell-free assay comprises contacting the NOVX protein or biologically-active portion thereof with a known compound which binds NOVX protein to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an NOVX protein, wherein determining the ability of the test compound to interact with an NOVX protein comprises determining the ability of the NOVX protein to preferentially bind to or modulate the activity of an NOVX target molecule.

The cell-free assays of the invention are amenable to use of both the soluble form or the membrane-bound form of NOVX protein. In the case of cell-free assays comprising the membrane-bound form of NOVX protein, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of NOVX protein is maintained in solution. Examples of 5 such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton® X-100, Triton® X-114, Thesit®, Isotridecypoly(ethylene glycol ether)_n, N-dodecyl-N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl) dimethyllamminiol-1-propane sulfonate (CHAPS), or 10 3-(3-cholamidopropyl)dimethyllamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the invention, it may be desirable to immobilize either NOVX protein or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to NOVX protein, or interaction of 15 NOVX protein with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For example, GST-NOVX fusion proteins or GST-target fusion proteins 20 can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or NOVX protein, and the mixture is incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to 25 remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described, *supra*. Alternatively, the complexes can be dissociated from the matrix, and the level of NOVX protein binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the 30 screening assays of the invention. For example, either the NOVX protein or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated NOVX protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well-known within the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well

plates (Pierce Chemical). Alternatively, antibodies reactive with NOVX protein or target molecules, but which do not interfere with binding of the NOVX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or NOVX protein trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the NOVX protein or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the NOVX protein or target molecule.

In another embodiment, modulators of NOVX protein expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of NOVX mRNA or protein in the cell is determined. The level of expression of NOVX mRNA or protein in the presence of the candidate compound is compared to the level of expression of NOVX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of NOVX mRNA or protein expression based upon this comparison. For example, when expression of NOVX mRNA or protein is greater (*i.e.*, statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of NOVX mRNA or protein expression. Alternatively, when expression of NOVX mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of NOVX mRNA or protein expression. The level of NOVX mRNA or protein expression in the cells can be determined by methods described herein for detecting NOVX mRNA or protein.

In yet another aspect of the invention, the NOVX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (*see, e.g.*, U.S. Patent No. 5,283,317; Zervos, *et al.*, 1993. *Cell* 72: 223-232; Madura, *et al.*, 1993. *J. Biol. Chem.* 268: 12046-12054; Bartel, *et al.*, 1993. *Biotechniques* 14: 920-924; Iwabuchi, *et al.*, 1993. *Oncogene* 8: 1693-1696; and Brent WO 94/10300), to identify other proteins that bind to or interact with NOVX ("NOVX-binding proteins" or "NOVX-bp") and modulate NOVX activity. Such NOVX-binding proteins are also likely to be involved in the propagation of signals by the NOVX proteins as, for example, upstream or downstream elements of the NOVX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for NOVX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the

other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming an NOVX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with NOVX.

The invention further pertains to novel agents identified by the aforementioned screening assays and uses thereof for treatments as described herein.

Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. By way of example, and not of limitation, these sequences can be used to: (*i*) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (*ii*) identify an individual from a minute biological sample (tissue typing); and (*iii*) aid in forensic identification of a biological sample. Some of these applications are described in the subsections, below.

20

Chromosome Mapping

Once the sequence (or a portion of the sequence) of a gene has been isolated, this sequence can be used to map the location of the gene on a chromosome. This process is called chromosome mapping. Accordingly, portions or fragments of the NOVX sequences, SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, or fragments or derivatives thereof, can be used to map the location of the NOVX genes, respectively, on a chromosome. The mapping of the NOVX sequences to chromosomes is an important first step in correlating these sequences with genes associated with disease.

Briefly, NOVX genes can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp in length) from the NOVX sequences. Computer analysis of the NOVX, sequences can be used to rapidly select primers that do not span more than one exon in the genomic DNA, thus complicating the amplification process. These primers can then be used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only

those hybrids containing the human gene corresponding to the NOVX sequences will yield an amplified fragment.

Somatic cell hybrids are prepared by fusing somatic cells from different mammals (e.g., human and mouse cells). As hybrids of human and mouse cells grow and divide, they 5 gradually lose human chromosomes in random order, but retain the mouse chromosomes. By using media in which mouse cells cannot grow, because they lack a particular enzyme, but in which human cells can, the one human chromosome that contains the gene encoding the needed enzyme will be retained. By using various media, panels of hybrid cell lines can be established. Each cell line in a panel contains either a single human chromosome or a small 10 number of human chromosomes, and a full set of mouse chromosomes, allowing easy mapping of individual genes to specific human chromosomes. *See, e.g., D'Eustachio, et al., 1983. Science 220: 919-924.* Somatic cell hybrids containing only fragments of human chromosomes can also be produced by using human chromosomes with translocations and deletions.

15 PCR mapping of somatic cell hybrids is a rapid procedure for assigning a particular sequence to a particular chromosome. Three or more sequences can be assigned per day using a single thermal cycler. Using the NOVX sequences to design oligonucleotide primers, sub-localization can be achieved with panels of fragments from specific chromosomes.

Fluorescence *in situ* hybridization (FISH) of a DNA sequence to a metaphase 20 chromosomal spread can further be used to provide a precise chromosomal location in one step. Chromosome spreads can be made using cells whose division has been blocked in metaphase by a chemical like colcemid that disrupts the mitotic spindle. The chromosomes can be treated briefly with trypsin, and then stained with Giemsa. A pattern of light and dark bands develops on each chromosome, so that the chromosomes can be identified individually. 25 The FISH technique can be used with a DNA sequence as short as 500 or 600 bases. However, clones larger than 1,000 bases have a higher likelihood of binding to a unique chromosomal location with sufficient signal intensity for simple detection. Preferably 1,000 bases, and more preferably 2,000 bases, will suffice to get good results at a reasonable amount of time. For a review of this technique, *see, Verma, et al., HUMAN CHROMOSOMES: A 30 MANUAL OF BASIC TECHNIQUES* (Pergamon Press, New York 1988).

Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on that chromosome, or panels of reagents can be used for marking multiple sites and/or multiple chromosomes. Reagents corresponding to noncoding regions of the genes actually are preferred for mapping purposes. Coding sequences are more

likely to be conserved within gene families, thus increasing the chance of cross hybridizations during chromosomal mapping.

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such 5 data are found, e.g., in McKusick, MENDELIAN INHERITANCE IN MAN, available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and disease, mapped to the same chromosomal region, can then be identified through linkage analysis (co-inheritance of physically adjacent genes), described in, e.g., Egeland, *et al.*, 1987. *Nature*, 325: 783-787.

10 Moreover, differences in the DNA sequences between individuals affected and unaffected with a disease associated with the NOVX gene, can be determined. If a mutation is observed in some or all of the affected individuals but not in any unaffected individuals, then the mutation is likely to be the causative agent of the particular disease. Comparison of affected and unaffected individuals generally involves first looking for structural alterations in 15 the chromosomes, such as deletions or translocations that are visible from chromosome spreads or detectable using PCR based on that DNA sequence. Ultimately, complete sequencing of genes from several individuals can be performed to confirm the presence of a mutation and to distinguish mutations from polymorphisms.

20 **Tissue Typing**

The NOVX sequences of the invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the invention are useful as additional DNA markers for RFLP 25 ("restriction fragment length polymorphisms," described in U.S. Patent No. 5,272,057).

Furthermore, the sequences of the invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the NOVX sequences described herein can be used to prepare two PCR primers from the 5'- and 3'-termini of the sequences. These primers can then be used to 30 amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the invention can be used to obtain such identification sequences from individuals and from tissue. The NOVX sequences

of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences, such as those in SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26 are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

15

Predictive Medicine

The invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the invention relates to diagnostic assays for determining NOVX protein and/or nucleic acid expression as well as NOVX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant NOVX expression or activity. The disorders include metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with NOVX protein, nucleic acid expression or activity. For example, mutations in an NOVX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with NOVX protein, nucleic acid expression, or biological activity.

Another aspect of the invention provides methods for determining NOVX protein, nucleic acid expression or activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (e.g., drugs) for therapeutic or 5 prophylactic treatment of an individual based on the genotype of the individual (e.g., the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (e.g., drugs, compounds) on the expression or activity of NOVX in clinical trials.

10 These and other agents are described in further detail in the following sections.

Diagnostic Assays

An exemplary method for detecting the presence or absence of NOVX in a biological sample involves obtaining a biological sample from a test subject and contacting the biological 15 sample with a compound or an agent capable of detecting NOVX protein or nucleic acid (e.g., mRNA, genomic DNA) that encodes NOVX protein such that the presence of NOVX is detected in the biological sample. An agent for detecting NOVX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to NOVX mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length NOVX nucleic acid, such as the nucleic 20 acid of SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to NOVX mRNA or genomic DNA. Other suitable probes for use in the diagnostic assays of the invention are described herein.

25 An agent for detecting NOVX protein is an antibody capable of binding to NOVX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (e.g., Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable 30 substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin. The term "biological sample" is intended to include tissues, cells and

biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect NOVX mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of NOVX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of NOVX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection of NOVX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of NOVX protein include introducing into a subject a labeled anti-NOVX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

10 In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

15 In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting NOVX protein, mRNA, or genomic DNA, such that the presence of NOVX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of NOVX protein, mRNA or genomic DNA in the control sample with the presence of NOVX protein, mRNA or genomic DNA in the test sample.

20 The invention also encompasses kits for detecting the presence of NOVX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting NOVX protein or mRNA in a biological sample; means for determining the amount of NOVX in the sample; and means for comparing the amount of NOVX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect NOVX protein or nucleic acid.

Prognostic Assays

25 The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant NOVX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with NOVX protein, nucleic acid expression or activity.

Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the invention provides a method for identifying a disease or disorder associated with aberrant NOVX expression or activity in which a test sample is obtained from a subject and NOVX protein or nucleic acid (e.g., mRNA, genomic DNA) is detected, wherein the presence of NOVX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant NOVX expression or activity. As used herein, a "test sample" refers to a biological sample obtained from a subject of interest. For example, a test sample can be a biological fluid (e.g., serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (e.g., an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant NOVX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder. Thus, the invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant NOVX expression or activity in which a test sample is obtained and NOVX protein or nucleic acid is detected (e.g., wherein the presence of NOVX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant NOVX expression or activity).

The methods of the invention can also be used to detect genetic lesions in an NOVX gene, thereby determining if a subject with the lesioned gene is at risk for a disorder characterized by aberrant cell proliferation and/or differentiation. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding an NOVX-protein, or the misexpression of the NOVX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of: (i) a deletion of one or more nucleotides from an NOVX gene; (ii) an addition of one or more nucleotides to an NOVX gene; (iii) a substitution of one or more nucleotides of an NOVX gene, (iv) a chromosomal rearrangement of an NOVX gene; (v) an alteration in the level of a messenger RNA transcript of an NOVX gene, (vi) aberrant modification of an NOVX gene, such as of the methylation pattern of the genomic DNA, (vii) the presence of a non-wild-type splicing pattern of a messenger RNA transcript of an NOVX gene, (viii) a non-wild-type level of an NOVX protein, (ix) allelic loss of an NOVX gene, and (x) inappropriate post-translational

modification of an NOVX protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in an NOVX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be
5 used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (*see, e.g.*, U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (*see, e.g.*, Landegran, *et al.*, 1988. *Science* 241: 1077-1080; and Nakazawa, *et al.*, 1994. *Proc. Natl. Acad. Sci. USA* 91: 360-364), the latter of which can be particularly useful for detecting point mutations in the NOVX-gene (*see, Abravaya, et al.*, 1995. *Nucl. Acids Res.* 23: 675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.*, genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to an NOVX gene
10 under conditions such that hybridization and amplification of the NOVX gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.
15

Alternative amplification methods include: self sustained sequence replication (*see, Guatelli, et al.*, 1990. *Proc. Natl. Acad. Sci. USA* 87: 1874-1878), transcriptional amplification system (*see, Kwoh, et al.*, 1989. *Proc. Natl. Acad. Sci. USA* 86: 1173-1177); Q β Replicase (*see, Lizardi, et al.*, 1988. *BioTechnology* 6: 1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to
20 those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.
25

In an alternative embodiment, mutations in an NOVX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction
30 endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (*see, e.g.*, U.S. Patent No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in NOVX can be identified by hybridizing a sample and control nucleic acids, e.g., DNA or RNA, to high-density arrays containing hundreds or thousands of oligonucleotides probes. See, e.g., Cronin, *et al.*, 1996. *Human Mutation* 7: 244-255; Kozal, *et al.*, 1996. *Nat. Med.* 2: 753-759. For example, genetic 5 mutations in NOVX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin, *et al.*, *supra*. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This is followed by a second 10 hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art 15 can be used to directly sequence the NOVX gene and detect mutations by comparing the sequence of the sample NOVX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert, 1977. *Proc. Natl. Acad. Sci. USA* 74: 560 or Sanger, 1977. *Proc. Natl. Acad. Sci. USA* 74: 5463. It is also contemplated that any of a variety of automated sequencing procedures 20 can be utilized when performing the diagnostic assays (see, e.g., Naeve, *et al.*, 1995. *Biotechniques* 19: 448), including sequencing by mass spectrometry (see, e.g., PCT International Publication No. WO 94/16101; Cohen, *et al.*, 1996. *Adv. Chromatography* 36: 127-162; and Griffin, *et al.*, 1993. *Appl. Biochem. Biotechnol.* 38: 147-159).

Other methods for detecting mutations in the NOVX gene include methods in which 25 protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA heteroduplexes. See, e.g., Myers, *et al.*, 1985. *Science* 230: 1242. In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type NOVX sequence with potentially 30 mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S₁ nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide

and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, e.g., Cotton, et al., 1988. *Proc. Natl. Acad. Sci. USA* 85: 4397; Saleeba, et al., 1992. *Methods Enzymol.* 217: 286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in NOVX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* 10 cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches. See, e.g., Hsu, et al., 1994. *Carcinogenesis* 15: 1657-1662. According to an exemplary embodiment, a probe based on an NOVX sequence, e.g., a wild-type NOVX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be 15 detected from electrophoresis protocols or the like. See, e.g., U.S. Patent No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in NOVX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids. See, e.g., Orita, et al., 1989. *Proc. Natl. Acad. Sci. USA*: 86: 2766; Cotton, 20 1993. *Mutat. Res.* 285: 125-144; Hayashi, 1992. *Genet. Anal. Tech. Appl.* 9: 73-79.

Single-stranded DNA fragments of sample and control NOVX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled 25 probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. See, e.g., Keen, et al., 1991. *Trends Genet.* 7: 5.

30 In yet another embodiment, the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). See, e.g., Myers, et al., 1985. *Nature* 313: 495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich

DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. *See, e.g., Rosenbaum and Reissner, 1987. Biophys. Chem. 265: 12753.*

Examples of other techniques for detecting point mutations include, but are not limited 5 to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. *See, e.g., Saiki, et al., 1986. Nature 324: 163; Saiki, et al., 1989. Proc. Natl. Acad. Sci. USA 86: 6230.* Such allele specific oligonucleotides 10 are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR 15 amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization; *see, e.g., Gibbs, et al., 1989. Nucl. Acids Res. 17: 2437-2448*) or at the extreme 3'-terminus of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (*see, e.g., Prossner, 1993. Tibtech. 11: 238*). In addition it may be desirable to introduce a novel 20 restriction site in the region of the mutation to create cleavage-based detection. *See, e.g., Gasparini, et al., 1992. Mol. Cell Probes 6: 1.* It is anticipated that in certain embodiments amplification may also be performed using *Taq* ligase for amplification. *See, e.g., Barany, 1991. Proc. Natl. Acad. Sci. USA 88: 189.* In such cases, ligation will occur only if there is a perfect match at the 3'-terminus of the 5' sequence, making it possible to detect the presence of 25 a known mutation at a specific site by looking for the presence or absence of amplification.

The methods described herein may be performed, for example, by utilizing 30 pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, e.g., in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving an NOVX gene.

Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which NOVX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

Pharmacogenomics

Agents, or modulators that have a stimulatory or inhibitory effect on NOVX activity (e.g., NOVX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (The disorders include metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.) In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (e.g., drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the activity of NOVX protein, expression of NOVX nucleic acid, or mutation content of NOVX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See e.g., Eichelbaum, 1996. *Clin. Exp. Pharmacol. Physiol.*, 23: 983-985; Linder, 1997. *Clin. Chem.*, 43: 254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic

polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are
5 expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side
10 effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. At the other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

15 Thus, the activity of NOVX protein, expression of NOVX nucleic acid, or mutation content of NOVX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness
20 phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with an NOVX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

25 **Monitoring of Effects During Clinical Trials**

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of NOVX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to
30 increase NOVX gene expression, protein levels, or upregulate NOVX activity, can be monitored in clinical trials of subjects exhibiting decreased NOVX gene expression, protein levels, or downregulated NOVX activity. Alternatively, the effectiveness of an agent determined by a screening assay to decrease NOVX gene expression, protein levels, or downregulate NOVX activity, can be monitored in clinical trials of subjects exhibiting

increased NOVX gene expression, protein levels, or upregulated NOVX activity. In such clinical trials, the expression or activity of NOVX and, preferably, other genes that have been implicated in, for example, a cellular proliferation or immune disorder can be used as a "read out" or markers of the immune responsiveness of a particular cell.

5 By way of example, and not of limitation, genes, including NOVX, that are modulated in cells by treatment with an agent (e.g., compound, drug or small molecule) that modulates NOVX activity (e.g., identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of
10 NOVX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of NOVX or other genes. In this manner, the gene expression pattern can serve as a marker, indicative of the physiological
15 response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (e.g., an agonist, antagonist, protein, peptide, peptidomimetic, nucleic acid, small molecule, or other drug candidate identified by the
20 screening assays described herein) comprising the steps of (*i*) obtaining a pre-administration sample from a subject prior to administration of the agent; (*ii*) detecting the level of expression of an NOVX protein, mRNA, or genomic DNA in the preadministration sample; (*iii*) obtaining one or more post-administration samples from the subject; (*iv*) detecting the level of expression or activity of the NOVX protein, mRNA, or genomic DNA in the
25 post-administration samples; (*v*) comparing the level of expression or activity of the NOVX protein, mRNA, or genomic DNA in the pre-administration sample with the NOVX protein, mRNA, or genomic DNA in the post administration sample or samples; and (*vi*) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of NOVX to higher levels
30 than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of NOVX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant NOVX expression or activity. The disorders include cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia, prostate cancer, neoplasm; adenocarcinoma, lymphoma, uterus cancer, fertility, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial asthma, Crohn's disease; multiple sclerosis, treatment of Albright Hereditary Osteodystrophy, and other diseases, disorders and conditions of the like.

These methods of treatment will be discussed more fully, below.

15 Disease and Disorders

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to: (i) an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to an aforementioned peptide; (iii) nucleic acids encoding an aforementioned peptide; (iv) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to an aforementioned peptide) that are utilized to "knockout" endogenous function of an aforementioned peptide by homologous recombination (see, e.g., Capecchi, 1989. *Science* 244: 1288-1292); or (v) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between an aforementioned peptide and its binding partner.

30 Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be

utilized include, but are not limited to, an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for 5 RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of an aforementioned peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in* 10 *situ* hybridization, and the like).

Prophylactic Methods

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant NOVX expression or activity, by administering to the 15 subject an agent that modulates NOVX expression or at least one NOVX activity. Subjects at risk for a disease that is caused or contributed to by aberrant NOVX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation 20 of symptoms characteristic of the NOVX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending upon the type of NOVX aberrancy, for example, an NOVX agonist or NOVX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein. The prophylactic methods of the invention are further discussed in the following subsections.

25

Therapeutic Methods

Another aspect of the invention pertains to methods of modulating NOVX expression or activity for therapeutic purposes. The modulatory method of the invention involves 30 contacting a cell with an agent that modulates one or more of the activities of NOVX protein activity associated with the cell. An agent that modulates NOVX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of an NOVX protein, a peptide, an NOVX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more NOVX protein activity. Examples of such stimulatory agents include active NOVX protein and a nucleic acid molecule encoding NOVX

that has been introduced into the cell. In another embodiment, the agent inhibits one or more NOVX protein activity. Examples of such inhibitory agents include antisense NOVX nucleic acid molecules and anti-NOVX antibodies. These modulatory methods can be performed *in vitro* (e.g., by culturing the cell with the agent) or, alternatively, *in vivo* (e.g., by administering the agent to a subject). As such, the invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of an NOVX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (e.g., an agent identified by a screening assay described herein), or combination of agents that modulates (e.g., up-regulates or down-regulates) NOVX expression or activity. In another embodiment, the method involves administering an NOVX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant NOVX expression or activity.

Stimulation of NOVX activity is desirable *in situations* in which NOVX is abnormally downregulated and/or in which increased NOVX activity is likely to have a beneficial effect. One example of such a situation is where a subject has a disorder characterized by aberrant cell proliferation and/or differentiation (e.g., cancer or immune associated disorders). Another example of such a situation is where the subject has a gestational disease (e.g., preclampsia).

Determination of the Biological Effect of the Therapeutic

In various embodiments of the invention, suitable *in vitro* or *in vivo* assays are performed to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

Prophylactic and Therapeutic Uses of the Compositions of the Invention

The NOVX nucleic acids and proteins of the invention are useful in potential prophylactic and therapeutic applications implicated in a variety of disorders including, but not limited to: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder,

immune disorders, hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.

As an example, a cDNA encoding the NOVX protein of the invention may be useful in gene therapy, and the protein may be useful when administered to a subject in need thereof. By way of non-limiting example, the compositions of the invention will have efficacy for treatment of patients suffering from: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, hematopoietic disorders, and the various dyslipidemias.

Both the novel nucleic acid encoding the NOVX protein, and the NOVX protein of the invention, or fragments thereof, may also be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. A further use could be as an anti-bacterial molecule (*i.e.*, some peptides have been found to possess anti-bacterial properties). These materials are further useful in the generation of antibodies, which immunospecifically-bind to the novel substances of the invention for use in therapeutic or diagnostic methods.

The invention will be further described in the following examples, which do not limit the scope of the invention described in the claims.

20

Examples

Example 1. Identification of NOVX clones

The novel NOVX target sequences identified in the present invention were subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. Table 11A shows the sequences of the PCR primers used for obtaining different clones. In each case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such primers were designed based on *in silico* predictions for the full length cDNA, part (one or more exons) of the DNA or protein sequence of the target sequence, or by translated homology of the predicted exons to closely related human sequences from other species. These primers were then employed in PCR amplification based

on the following pool of human cDNAs: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea, uterus. Usually the resulting amplicons were gel purified, cloned and sequenced to high redundancy. The PCR product derived from exon linking was cloned into the pCR2.1 vector from Invitrogen. The resulting bacterial clone has an insert covering the entire open reading frame cloned into the pCR2.1 vector. Table 17B shows a list of these bacterial clones. The resulting sequences from all clones were assembled with themselves, with other fragments in CuraGen Corporation's database and with public ESTs. Fragments and ESTs were included as components for an assembly when the extent of their identity with another component of the assembly was at least 95% over 50 bp. In addition, sequence traces were evaluated manually and edited for corrections if appropriate. These procedures provide the sequence reported herein.

15

Table 11A. PCR Primers for Exon Linking

NOVX Clone	Primer 1 (5' - 3')	SEQ ID NO	Primer 2 (5' - 3')	SEQ ID NO
NOV1c	TCATCACATGACAAACATGAAGCTGT	87	GAAAGCCCTCAAACCTCTCCATCTATG	88
NOV7a	CCAATCTCTGATGCCCTGCGAT	89	AGGTCAGTGCCGGAGCCTCC	90

Physical clone: Exons were predicted by homology and the intron/exon boundaries were determined using standard genetic rules. Exons were further selected and refined by means of similarity determination using multiple BLAST (for example, tBlastN, BlastX, and BlastN) searches, and, in some instances, GeneScan and Grail. Expressed sequences from both public and proprietary databases were also added when available to further define and complete the gene sequence. The DNA sequence was then manually corrected for apparent inconsistencies thereby obtaining the sequences encoding the full-length protein.

Table 11B. Physical Clones for PCR products

NOVX Clone	Bacterial Clone
NOV1	Physical clone: 128940::83420733.698715.E24
NOV2	Physical clone: AL357059, AL022344, AL3555530, AL356100, AC016042
NOV4	Physical clone: AC009785
NOV5	Genomic clone: GMChromosome4
NOV7a	Genomic file: gb_AC010319 HTG Homo sapiens chromosome 19 CTD-2521M24
NOV8	Physical clone: AC008803, AC010449, AC026718

25

Example 2. Quantitative expression analysis of clones in various cells and tissues

The quantitative expression of various clones was assessed using microtiter plates containing RNA samples from a variety of normal and pathology-derived cells, cell lines and tissues using real time quantitative PCR (RTQ PCR). RTQ PCR was performed on a Perkin-Elmer Biosystems ABI PRISM® 7700 Sequence Detection System. Various collections of 5 samples are assembled on the plates, and referred to as Panel 1 (containing normal tissues and cancer cell lines), Panel 2 (containing samples derived from tissues from normal and cancer sources), Panel 3 (containing cancer cell lines), Panel 4 (containing cells and cell lines from normal tissues and cells related to inflammatory conditions), AI_comprehensive_panel (containing normal tissue and samples from autoinflammatory diseases), Panel CNSD.01 10 (containing samples from normal and diseased brains) and CNS_neurodegeneration_panel (containing samples from normal and diseased brains).

First, the RNA samples were normalized to reference nucleic acids such as constitutively expressed genes (for example, β -actin and GAPDH). Normalized RNA (5 μ l) was converted to cDNA and analyzed by RTQ-PCR using One Step RT-PCR Master Mix 15 Reagents (PE Biosystems; Catalog No. 4309169) and gene-specific primers according to the manufacturer's instructions. Probes and primers were designed for each assay according to Perkin Elmer Biosystem's *Primer Express* Software package (version I for Apple Computer's Macintosh Power PC) or a similar algorithm using the target sequence as input. Default settings were used for reaction conditions and the following parameters were set before 20 selecting primers: primer concentration = 250 nM, primer melting temperature (T_m) range = 58°-60° C, primer optimal T_m = 59° C, maximum primer difference = 2° C, probe does not have 5' G, probe T_m must be 10° C greater than primer T_m , amplicon size 75 bp to 100 bp. The probes and primers selected (see below) were synthesized by Synthegen (Houston, TX, USA). Probes were double purified by HPLC to remove uncoupled dye and evaluated by 25 mass spectroscopy to verify coupling of reporter and quencher dyes to the 5' and 3' ends of the probe, respectively. Their final concentrations were: forward and reverse primers, 900 nM each, and probe, 200nM.

PCR conditions: Normalized RNA from each tissue and each cell line was spotted in each well of a 96 well PCR plate (Perkin Elmer Biosystems). PCR cocktails including two 30 probes (a probe specific for the target clone and another gene-specific probe multiplexed with the target probe) were set up using 1X TaqMan™ PCR Master Mix for the PE Biosystems 7700, with 5 mM MgCl₂, dNTPs (dA, G, C, U at 1:1:1:2 ratios), 0.25 U/ml AmpliTaq Gold™ (PE Biosystems), and 0.4 U/ μ l RNase inhibitor, and 0.25 U/ μ l reverse transcriptase. Reverse transcription was performed at 48° C for 30 minutes followed by amplification/PCR cycles as

follows: 95° C 10 min, then 40 cycles of 95° C for 15 seconds, 60° C for 1 minute. Results were recorded as CT values (cycle at which a given sample crosses a threshold level of fluorescence) using a log scale, with the difference in RNA concentration between a given sample and the sample with the lowest CT value being represented as 2 to the power of delta CT. The percent relative expression is then obtained by taking the reciprocal of this RNA difference and multiplying by 100.

Panel 1

In the results for Panel 1, the following abbreviations are used:

ca. = carcinoma,
* = established from metastasis,
met = metastasis,
s cell var = small cell variant,
non-s = non-sm = non-small,
squam = squamous,
pl. eff = pl effusion = pleural effusion,
glio = glioma,
astro = astrocytoma, and
neuro = neuroblastoma.

Panel 2

The plates for Panel 2 generally include 2 control wells and 94 test samples composed of RNA or cDNA isolated from human tissue procured by surgeons working in close cooperation with the National Cancer Institute's Cooperative Human Tissue Network (CHTN) or the National Disease Research Initiative (NDRI). The tissues are derived from human malignancies and in cases where indicated many malignant tissues have "matched margins" obtained from noncancerous tissue just adjacent to the tumor. These are termed normal adjacent tissues and are denoted "NAT" in the results below. The tumor tissue and the "matched margins" are evaluated by two independent pathologists (the surgical pathologists and again by a pathologists at NDRI or CHTN). This analysis provides a gross histopathological assessment of tumor differentiation grade. Moreover, most samples include the original surgical pathology report that provides information regarding the clinical stage of

the patient. These matched margins are taken from the tissue surrounding (i.e. immediately proximal) to the zone of surgery (designated "NAT", for normal adjacent tissue, in Table RR). In addition, RNA and cDNA samples were obtained from various human tissues derived from autopsies performed on elderly people or sudden death victims (accidents, etc.). These tissues
5 were ascertained to be free of disease and were purchased from various commercial sources such as Clontech (Palo Alto, CA), Research Genetics, and Invitrogen.

RNA integrity from all samples is controlled for quality by visual assessment of agarose gel electropherograms using 28S and 18S ribosomal RNA staining intensity ratio as a guide (2:1 to 2.5:1 28s:18s) and the absence of low molecular weight RNAs that would be
10 indicative of degradation products. Samples are controlled against genomic DNA contamination by RTQ PCR reactions run in the absence of reverse transcriptase using probe and primer sets designed to amplify across the span of a single exon.

Panel 3D

The plates of Panel 3D are comprised of 94 cDNA samples and two control samples.
15 Specifically, 92 of these samples are derived from cultured human cancer cell lines, 2 samples of human primary cerebellar tissue and 2 controls. The human cell lines are generally obtained from ATCC (American Type Culture Collection), NCI or the German tumor cell bank and fall into the following tissue groups: Squamous cell carcinoma of the tongue, breast cancer, prostate cancer, melanoma, epidermoid carcinoma, sarcomas, bladder carcinomas,
20 pancreatic cancers, kidney cancers, leukemias/lymphomas, ovarian/uterine/cervical, gastric, colon, lung and CNS cancer cell lines. In addition, there are two independent samples of cerebellum. These cells are all cultured under standard recommended conditions and RNA extracted using the standard procedures. The cell lines in panel 3D and 1.3D are of the most common cell lines used in the scientific literature.

25 RNA integrity from all samples is controlled for quality by visual assessment of agarose gel electropherograms using 28S and 18S ribosomal RNA staining intensity ratio as a guide (2:1 to 2.5:1 28s:18s) and the absence of low molecular weight RNAs that would be indicative of degradation products. Samples are controlled against genomic DNA contamination by RTQ PCR reactions run in the absence of reverse transcriptase using probe
30 and primer sets designed to amplify across the span of a single exon.

Panel 4

Panel 4 includes samples on a 96 well plate (2 control wells, 94 test samples) composed of RNA (Panel 4r) or cDNA (Panel 4d) isolated from various human cell lines or tissues related to inflammatory conditions. Total RNA from control normal tissues such as colon and lung (Stratagene ,La Jolla, CA) and thymus and kidney (Clontech) were employed.

5 Total RNA from liver tissue from cirrhosis patients and kidney from lupus patients was obtained from BioChain (Biochain Institute, Inc., Hayward, CA). Intestinal tissue for RNA preparation from patients diagnosed as having Crohn's disease and ulcerative colitis was obtained from the National Disease Research Interchange (NDRI) (Philadelphia, PA).

Astrocytes, lung fibroblasts, dermal fibroblasts, coronary artery smooth muscle cells, 10 small airway epithelium, bronchial epithelium, microvascular dermal endothelial cells, microvascular lung endothelial cells, human pulmonary aortic endothelial cells, human umbilical vein endothelial cells were all purchased from Clonetics (Walkersville, MD) and grown in the media supplied for these cell types by Clonetics. These primary cell types were activated with various cytokines or combinations of cytokines for 6 and/or 12-14 hours, as 15 indicated. The following cytokines were used; IL-1 beta at approximately 1-5 ng/ml, TNF alpha at approximately 5-10 ng/ml, IFN gamma at approximately 20-50 ng/ml, IL-4 at approximately 5-10 ng/ml, IL-9 at approximately 5-10 ng/ml, IL-13 at approximately 5-10 ng/ml. Endothelial cells were sometimes starved for various times by culture in the basal media from Clonetics with 0.1% serum.

20 Mononuclear cells were prepared from blood of employees at CuraGen Corporation, using Ficoll. LAK cells were prepared from these cells by culture in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco/Life Technologies, Rockville, MD), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and Interleukin 2 for 4-6 days. Cells were then either activated with 10-20 ng/ml 25 PMA and 1-2 µg/ml ionomycin, IL-12 at 5-10 ng/ml, IFN gamma at 20-50 ng/ml and IL-18 at 5-10 ng/ml for 6 hours. In some cases, mononuclear cells were cultured for 4-5 days in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) with PHA (phytohemagglutinin) or PWM (pokeweed mitogen) at approximately 5 µg/ml. Samples 30 were taken at 24, 48 and 72 hours for RNA preparation. MLR (mixed lymphocyte reaction) samples were obtained by taking blood from two donors, isolating the mononuclear cells using Ficoll and mixing the isolated mononuclear cells 1:1 at a final concentration of approximately 2×10^6 cells/ml in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol (5.5×10^{-5} M) (Gibco), and 10 mM Hepes

(Gibco). The MLR was cultured and samples taken at various time points ranging from 1- 7 days for RNA preparation.

Monocytes were isolated from mononuclear cells using CD14 Miltenyi Beads, +ve VS selection columns and a Vario Magnet according to the manufacturer's instructions.

- 5 Monocytes were differentiated into dendritic cells by culture in DMEM 5% fetal calf serum (FCS) (Hyclone, Logan, UT), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco), 50 ng/ml GMCSF and 5 ng/ml IL-4 for 5-7 days. Macrophages were prepared by culture of monocytes for 5-7 days in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco) and 10% AB Human Serum or MCSF at approximately 50 ng/ml. Monocytes, macrophages and dendritic cells were stimulated for 6 and 12-14 hours with lipopolysaccharide (LPS) at 100 ng/ml. Dendritic cells were also stimulated with anti-CD40 monoclonal antibody (Pharmingen) at 10 µg/ml for 6 and 12-14 hours.
- 10
- 15 CD4 lymphocytes, CD8 lymphocytes and NK cells were also isolated from mononuclear cells using CD4, CD8 and CD56 Miltenyi beads, positive VS selection columns and a Vario Magnet according to the manufacturer's instructions. CD45RA and CD45RO CD4 lymphocytes were isolated by depleting mononuclear cells of CD8, CD56, CD14 and CD19 cells using CD8, CD56, CD14 and CD19 Miltenyi beads and positive selection. Then
- 20 CD45RO beads were used to isolate the CD45RO CD4 lymphocytes with the remaining cells being CD45RA CD4 lymphocytes. CD45RA CD4, CD45RO CD4 and CD8 lymphocytes were placed in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and plated at 10^6 cells/ml onto Falcon 6 well tissue culture plates that had been coated
- 25 overnight with 0.5 µg/ml anti-CD28 (Pharmingen) and 3 ug/ml anti-CD3 (OKT3, ATCC) in PBS. After 6 and 24 hours, the cells were harvested for RNA preparation. To prepare chronically activated CD8 lymphocytes, we activated the isolated CD8 lymphocytes for 4 days on anti-CD28 and anti-CD3 coated plates and then harvested the cells and expanded them in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium
- 30 pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and IL-2. The expanded CD8 cells were then activated again with plate bound anti-CD3 and anti-CD28 for 4 days and expanded as before. RNA was isolated 6 and 24 hours after the second activation and after 4 days of the second expansion culture. The isolated NK cells were cultured in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM

sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and IL-2 for 4-6 days before RNA was prepared.

To obtain B cells, tonsils were procured from NDRI. The tonsil was cut up with sterile dissecting scissors and then passed through a sieve. Tonsil cells were then spun down and resuspended at 10^6 cells/ml in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco). To activate the cells, we used PWM at 5 µg/ml or anti-CD40 (Pharmingen) at approximately 10 µg/ml and IL-4 at 5-10 ng/ml. Cells were harvested for RNA preparation at 24, 48 and 72 hours.

To prepare the primary and secondary Th1/Th2 and Tr1 cells, six-well Falcon plates were coated overnight with 10 µg/ml anti-CD28 (Pharmingen) and 2 µg/ml OKT3 (ATCC), and then washed twice with PBS. Umbilical cord blood CD4 lymphocytes (Poietic Systems, German Town, MD) were cultured at 10^5 - 10^6 cells/ml in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco) and IL-2 (4 ng/ml). IL-12 (5 ng/ml) and anti-IL4 (1 µg/ml) were used to direct to Th1, while IL-4 (5 ng/ml) and anti-IFN gamma (1 µg/ml) were used to direct to Th2 and IL-10 at 5 ng/ml was used to direct to Tr1. After 4-5 days, the activated Th1, Th2 and Tr1 lymphocytes were washed once in DMEM and expanded for 4-7 days in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco) and IL-2 (1 ng/ml). Following this, the activated Th1, Th2 and Tr1 lymphocytes were re-stimulated for 5 days with anti-CD28/OKT3 and cytokines as described above, but with the addition of anti-CD95L (1 µg/ml) to prevent apoptosis. After 4-5 days, the Th1, Th2 and Tr1 lymphocytes were washed and then expanded again with IL-2 for 4-7 days. Activated Th1 and Th2 lymphocytes were maintained in this way for a maximum of three cycles. RNA was prepared from primary and secondary Th1, Th2 and Tr1 after 6 and 24 hours following the second and third activations with plate bound anti-CD3 and anti-CD28 mAbs and 4 days into the second and third expansion cultures in Interleukin 2.

The following leukocyte cell lines were obtained from the ATCC: Ramos, EOL-1, KU-812. EOL cells were further differentiated by culture in 0.1 mM dbcAMP at 5×10^5 cells/ml for 8 days, changing the media every 3 days and adjusting the cell concentration to 5×10^5 cells/ml. For the culture of these cells, we used DMEM or RPMI (as recommended by the ATCC), with the addition of 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM

Hepes (Gibco). RNA was either prepared from resting cells or cells activated with PMA at 10 ng/ml and ionomycin at 1 µg/ml for 6 and 14 hours. Keratinocyte line CCD106 and an airway epithelial tumor line NCI-H292 were also obtained from the ATCC. Both were cultured in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco).

5 CCD1106 cells were activated for 6 and 14 hours with approximately 5 ng/ml TNF alpha and 1 ng/ml IL-1 beta, while NCI-H292 cells were activated for 6 and 14 hours with the following cytokines: 5 ng/ml IL-4, 5 ng/ml IL-9, 5 ng/ml IL-13 and 25 ng/ml IFN gamma.

For these cell lines and blood cells, RNA was prepared by lysing approximately 10^7 10 cells/ml using Trizol (Gibco BRL). Briefly, 1/10 volume of bromochloropropene (Molecular Research Corporation) was added to the RNA sample, vortexed and after 10 minutes at room temperature, the tubes were spun at 14,000 rpm in a Sorvall SS34 rotor. The aqueous phase was removed and placed in a 15 ml Falcon Tube. An equal volume of isopropanol was added and left at -20 degrees C overnight. The precipitated RNA was spun down at 9,000 rpm for 15 15 min in a Sorvall SS34 rotor and washed in 70% ethanol. The pellet was redissolved in 300 µl of RNase-free water and 35 µl buffer (Promega) 5 µl DTT, 7 µl RNAsin and 8 µl DNase were added. The tube was incubated at 37 degrees C for 30 minutes to remove contaminating genomic DNA, extracted once with phenol chloroform and re-precipitated with 1/10 volume of 3 M sodium acetate and 2 volumes of 100% ethanol. The RNA was spun down and placed 20 in RNase free water. RNA was stored at -80 degrees C.

Panel CNSD.01

The plates for Panel CNSD.01 include two control wells and 94 test samples 25 comprised of cDNA isolated from postmortem human brain tissue obtained from the Harvard Brain Tissue Resource Center. Brains are removed from calvaria of donors between 4 and 24 hours after death, sectioned by neuroanatomists, and frozen at -80°C in liquid nitrogen vapor. All brains are sectioned and examined by neuropathologists to confirm diagnoses with clear associated neuropathology.

30 Disease diagnoses are taken from patient records. The panel contains two brains from each of the following diagnoses: Alzheimer's disease, Parkinson's disease, Huntington's disease, Progressive Supernuclear Palsy, Depression, and "Normal controls". Within each of these brains, the following regions are represented: cingulate gyrus, temporal pole, globus palladus, substantia nigra, Brodmann Area 4 (primary motor strip), Brodmann Area 7 (parietal

cortex), Brodmann Area 9 (prefrontal cortex), and Brodmann area 17 (occipital cortex). Not all brain regions are represented in all cases; e.g., Huntington's disease is characterized in part by neurodegeneration in the globus pallidus, thus this region is impossible to obtain from confirmed Huntington's cases. Likewise Parkinson's disease is characterized by degeneration of the substantia nigra making this region more difficult to obtain. Normal control brains were examined for neuropathology and found to be free of any pathology consistent with neurodegeneration.

RNA integrity from all samples is controlled for quality by visual assessment of agarose gel electropherograms using 28S and 18S ribosomal RNA staining intensity ratio as a guide (2:1 to 2.5:1 28s:18s) and the absence of low molecular weight RNAs that would be indicative of degradation products. Samples are controlled against genomic DNA contamination by RTQ PCR reactions run in the absence of reverse transcriptase using probe and primer sets designed to amplify across the span of a single exon.

In the labels employed to identify tissues in the CNS panel, the following abbreviations are used:

PSP = Progressive supranuclear palsy
Sub Nigra = Substantia nigra
Glob Palladus= Globus pallidus
Temp Pole = Temporal pole
Cing Gyr = Cingulate gyrus
BA 4 = Brodmann Area 4

Panel CNS_Neurodegeneration_V1.0

The plates for Panel CNS_Neurodegeneration_V1.0 include two control wells and 47 test samples comprised of cDNA isolated from postmortem human brain tissue obtained from the Harvard Brain Tissue Resource Center (McLean Hospital) and the Human Brain and Spinal Fluid Resource Center (VA Greater Los Angeles Healthcare System). Brains are removed from calvaria of donors between 4 and 24 hours after death, sectioned by neuroanatomists, and frozen at -80°C in liquid nitrogen vapor. All brains are sectioned and examined by neuropathologists to confirm diagnoses with clear associated neuropathology.

Disease diagnoses are taken from patient records. The panel contains six brains from Alzheimer's disease (AD) patients, and eight brains from "Normal controls" who showed no evidence of dementia prior to death. The eight normal control brains are divided into two categories: Controls with no dementia and no Alzheimer's like pathology (Controls) and

controls with no dementia but evidence of severe Alzheimer's like pathology, (specifically senile plaque load rated as level 3 on a scale of 0-3; 0 = no evidence of plaques, 3 = severe AD senile plaque load). Within each of these brains, the following regions are represented: Hippocampus, Temporal cortex (Brodmann Area 21), Somatosensory cortex (Brodmann area 7), and Occipital cortex (Brodmann area 17). These regions were chosen to encompass all levels of neurodegeneration in AD. The hippocampus is a region of early and severe neuronal loss in AD; the temporal cortex is known to show neurodegeneration in AD after the hippocampus; the somatosensory cortex shows moderate neuronal death in the late stages of the disease; the occipital cortex is spared in AD and therefore acts as a "control" region within 10 AD patients. Not all brain regions are represented in all cases.

RNA integrity from all samples is controlled for quality by visual assessment of agarose gel electropherograms using 28S and 18S ribosomal RNA staining intensity ratio as a guide (2:1 to 2.5:1 28s:18s) and the absence of low molecular weight RNAs that would be indicative of degradation products. Samples are controlled against genomic DNA 15 contamination by RTQ PCR reactions run in the absence of reverse transcriptase using probe and primer sets designed to amplify across the span of a single exon.

In the labels employed to identify tissues in the CNS_Neurodegeneration_V1.0 panel, the following abbreviations are used:

AD = Alzheimer's disease brain; patient was demented and showed AD-like pathology
20 upon autopsy
Control = Control brains; patient not demented, showing no neuropathology
Control (Path) = Control brains; patient not demented but showing sever AD-like pathology
SupTemporal Ctx = Superior Temporal Cortex
25 Inf Temporal Ctx = Inferior Temporal Cortex

NOV1a

Expression of gene NOV1a was assessed using the primer-probe sets Ag273b and
30 Ag1094, described in Tables 12 and 13. Results from RTQ-PCR runs are shown in Tables 14,
15, 16, 17, and 18.

Table 12. Probe Name Ag273b

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-CGGCTTGACGGATGCCAC-3'		19	13	91
Probe	FAM-5'- TGA CTT CTGGG CTT ACCA AT GCT ATT CAA- 3'-TAMRA		32	37	92
Reverse	5'-GCACCTATCTCAATATCTGCAATATTG-3'		27	85	93

Table 13. Probe Name Ag1094

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-ATGGACTGGAAAACCTGGAA-3'	59.4	20	192	94
Probe	FAM-5'- TCCTGCAAGCAGATAACAATTATCACAA- 3'-TAMRA	66.5	29	213	95
Reverse	5'-TGCTAAAGGCACTTGGTTCA-3'	59.5	20	247	96

5

Table 14. Panel 1

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	tm566f ag273b		tm566f ag273b
Endothelial cells	0.0	Renal ca. 786-0	0.0
Endothelial cells (treated)	0.0	Renal ca. A498	0.0
Pancreas	0.0	Renal ca. RXF 393	0.0
Pancreatic ca. CAPAN 2	0.0	Renal ca. ACHN	0.0
Adrenal gland	0.0	Renal ca. UO-31	0.0
Thyroid	0.0	Renal ca. TK-10	0.0
Salavary gland	12.9	Liver	0.0
Pituitary gland	0.0	Liver (fetal)	0.0
Brain (fetal)	0.0	Liver ca. (hepatoblast) HepG2	0.0
Brain (whole)	0.2	Lung	0.5
Brain (amygdala)	0.0	Lung (fetal)	2.2
Brain (cerebellum)	1.6	Lung ca. (small cell) LX-1	0.0
Brain (hippocampus)	0.0	Lung ca. (small cell) NCI-H69	2.7
Brain (substantia nigra)	0.0	Lung ca. (s.cell var.) SHP-77	44.1
Brain (thalamus)	2.9	Lung ca. (large cell) NCI-H460	0.0
Brain (hypothalamus)	0.0	Lung ca. (non-sm. cell) A549	0.0
Spinal cord	0.0	Lung ca. (non-s.cell) NCI-H23	14.7
CNS ca. (glio/astro) U87-MG	0.0	Lung ca (non-s.cell) HOP-62	12.2
CNS ca. (glio/astro) U-118-MG	0.0	Lung ca. (non-s.cl) NCI-H522	0.2
CNS ca. (astro) SW1783	0.0	Lung ca. (squam.) SW 900	11.9
CNS ca.* (neuro; met) SK-N-AS	6.6	Lung ca. (squam.) NCI-H596	2.5
CNS ca. (astro) SF-539	0.0	Mammary gland	4.8

CNS ca. (astro) SNB-75	10.2	Breast ca.* (pl. effusion) MCF-7	0.4
CNS ca. (glio) SNB-19	24.3	Breast ca.* (plef) MDA-MB-231	0.0
CNS ca. (glio) U251	4.2	Breast ca.* (pl. effusion) T47D	7.2
CNS ca. (glio) SF-295	37.6	Breast ca. BT-549	0.0
Heart	1.5	Breast ca. MDA-N	0.0
Skeletal muscle	0.0	Ovary	0.0
Bone marrow	0.0	Ovarian ca. OVCAR-3	0.0
Thymus	0.4	Ovarian ca. OVCAR-4	0.0
Spleen	0.0	Ovarian ca. OVCAR-5	6.2
Lymph node	0.0	Ovarian ca. OVCAR-8	0.0
Colon (ascending)	9.9	Ovarian ca. IGROV-1	0.0
Stomach	0.4	Ovarian ca.* (ascites) SK-OV-3	0.0
Small intestine	4.2	Uterus	0.0
Colon ca. SW480	0.0	Placenta	0.8
Colon ca.* (SW480 met)SW620	0.0	Prostate	3.6
Colon ca. HT29	34.4	Prostate ca.* (bone met)PC-3	100.0
Colon ca. HCT-116	0.0	Testis	0.0
Colon ca. CaCo-2	0.0	Melanoma Hs688(A).T	0.0
Colon ca. HCT-15	0.0	Melanoma* (met) Hs688(B).T	0.0
Colon ca. HCC-2998	0.0	Melanoma UACC-62	0.3
Gastric ca.* (liver met) NCI-N87	1.3	Melanoma M14	0.0
Bladder	0.1	Melanoma LOX IMVI	0.0
Trachea	8.9	Melanoma* (met) SK-MEL-5	0.0
Kidney	0.2	Melanoma SK-MEL-28	0.2
Kidney (fetal)	1.3		

Table 15. Panel 1.3D

Tissue Name	Relative Expression(%)	
	1.3Dtm2741f_ag1094	1.3Dtm2838f_ag1094
Liver adenocarcinoma	10.0	9.1
Pancreas	0.2	0.1
Pancreatic ca. CAPAN 2	0.0	0.0
Adrenal gland	0.0	0.0
Thyroid	0.2	0.2
Salivary gland	8.9	4.3
Pituitary gland	0.0	0.2
Brain (fetal)	0.1	0.0
Brain (whole)	0.8	0.6
Brain (amygdala)	0.2	0.1
Brain (cerebellum)	0.5	0.7

Brain (hippocampus)	0.4	0.2
Brain (substantia nigra)	0.0	0.0
Brain (thalamus)	1.1	1.0
Cerebral Cortex	0.2	0.1
Spinal cord	0.2	0.0
CNS ca. (glio/astro) U87-MG	0.0	0.2
CNS ca. (glio/astro) U-118-MG	1.0	0.8
CNS ca. (astro) SW1783	1.1	0.9
CNS ca.* (neuro; met) SK-N-AS	26.4	26.8
CNS ca. (astro) SF-539	0.0	0.0
CNS ca. (astro) SNB-75	15.1	12.9
CNS ca. (glio) SNB-19	38.2	21.0
CNS ca. (glio) U251	3.3	3.7
CNS ca. (glio) SF-295	38.4	36.9
Heart (fetal)	0.2	0.5
Heart	0.6	0.3
Fetal Skeletal	2.9	2.2
Skeletal muscle	0.0	0.0
Bone marrow	0.0	0.2
Thymus	0.4	0.1
Spleen	0.0	0.0
Lymph node	0.0	0.0
Colorectal	1.6	0.6
Stomach	1.6	1.6
Small intestine	4.2	3.7
Colon ca. SW480	0.0	0.0
Colon ca.* (SW480 met) SW620	0.4	0.1
Colon ca. HT29	21.0	25.5
Colon ca. HCT-116	0.0	0.0
Colon ca. CaCo-2	0.0	0.0
83219 CC Well to Mod Diff (ODO3866)	0.0	0.0
Colon ca. HCC-2998	0.0	0.0
Gastric ca.* (liver met) NCI-N87	21.3	20.7
Bladder	0.1	0.0
Trachea	12.5	12.9
Kidney	0.0	0.0
Kidney (fetal)	0.9	0.6
Renal ca. 786-0	0.0	0.0
Renal ca. A498	2.0	1.5
Renal ca. RXF 393	0.0	0.0
Renal ca. ACHN	0.0	0.0
Renal ca. UO-31	0.0	0.0
Renal ca. TK-10	0.0	0.0
Liver	0.4	0.6
Liver (fetal)	1.6	1.0

Tissue Name	Relative Expression(%)	
Tissue Name	2Dtm2837f_ag1094	2dtm2940f_ag1094
Liver ca. (hepatoblast) HepG2	0.0	0.0
Lung	1.8	1.4
Lung (fetal)	11.7	7.5
Lung ca. (small cell) LX-1	0.2	0.0
Lung ca. (small cell) NCI-H69	2.4	3.1
Lung ca. (s.cell var.) SHP-77	100.0	100.0
Lung ca. (large cell)NCI-H460	0.0	0.0
Lung ca. (non-sm. cell) A549	0.3	0.8
Lung ca. (non-s.cell) NCI-H23	12.8	12.8
Lung ca (non-s.cell) HOP-62	3.9	3.7
Lung ca. (non-s.cl) NCI-H522	0.1	0.0
Lung ca. (squam.) SW 900	4.8	6.4
Lung ca. (squam.) NCI-H596	1.3	0.9
Mammary gland	3.4	3.3
Breast ca.* (pl. effusion) MCF-7	1.2	0.7
Breast ca.* (pl.ef) MDA-MB-231	0.0	0.0
Breast ca.* (pl. effusion) T47D	3.2	3.0
Breast ca. BT-549	2.1	1.7
Breast ca. MDA-N	0.0	0.0
Ovary	0.7	0.3
Ovarian ca. OVCAR-3	0.4	0.3
Ovarian ca. OVCAR-4	0.1	0.0
Ovarian ca. OVCAR-5	8.5	6.2
Ovarian ca. OVCAR-8	0.0	0.0
Ovarian ca. IGROV-1	0.0	0.0
Ovarian ca.* (ascites) SK-OV-3	0.3	0.2
Uterus	0.4	0.2
Placenta	1.0	1.3
Prostate	1.1	1.1
Prostate ca.* (bone met)PC-3	13.2	13.9
Testis	0.3	0.4
Melanoma Hs688(A).T	0.0	0.0
Melanoma* (met) Hs688(B).T	0.0	0.0
Melanoma UACC-62	0.0	0.0
Melanoma M14	0.0	0.0
Melanoma LOX IMVI	0.0	0.0
Melanoma* (met) SK-MEL-5	0.1	0.5
Adipose	0.5	0.4

Table 16. Panel 2D

Tissue Name	Relative Expression(%)	
	2Dtm2837f_ag1094	2dtm2940f_ag1094

Normal Colon GENPAK 061003	12.4	11.4
83219 CC Well to Mod Diff (ODO3866)	0.0	0.0
83220 CC NAT (ODO3866)	1.0	1.5
83221 CC Gr.2 rectosigmoid (ODO3868)	0.3	0.0
83222 CC NAT (ODO3868)	0.4	0.2
83235 CC Mod Diff (ODO3920)	0.0	0.0
83236 CC NAT (ODO3920)	0.8	0.8
83237 CC Gr.2 ascend colon (ODO3921)	2.4	2.2
83238 CC NAT (ODO3921)	2.0	1.9
83241 CC from Partial Hepatectomy (ODO4309)	0.0	0.0
83242 Liver NAT (ODO4309)	0.2	0.3
87472 Colon mets to lung (OD04451-01)	0.0	0.0
87473 Lung NAT (OD04451-02)	0.9	0.6
Normal Prostate Clontech A+ 6546-1	2.7	3.0
84140 Prostate Cancer (OD04410)	1.5	1.4
84141 Prostate NAT (OD04410)	6.5	8.0
87073 Prostate Cancer (OD04720-01)	5.9	6.1
87074 Prostate NAT (OD04720-02)	14.1	12.6
Normal Lung GENPAK 061010	3.3	3.5
83239 Lung Met to Muscle (ODO4286)	0.2	0.2
83240 Muscle NAT (ODO4286)	0.0	0.0
84136 Lung Malignant Cancer (OD03126)	7.9	6.0
84137 Lung NAT (OD03126)	1.8	2.5
84871 Lung Cancer (OD04404)	24.8	21.6
84872 Lung NAT (OD04404)	1.8	1.7
84875 Lung Cancer (OD04565)	0.7	1.2
84876 Lung NAT (OD04565)	0.5	0.7
85950 Lung Cancer (OD04237-01)	13.5	12.5
85970 Lung NAT (OD04237-02)	1.4	1.0
83255 Ocular Mel Met to Liver (ODO4310)	0.0	0.0
83256 Liver NAT (ODO4310)	0.2	0.4
84139 Melanoma Mets to Lung (OD04321)	0.4	0.2
84138 Lung NAT (OD04321)	2.5	1.2
Normal Kidney GENPAK 061008	0.2	0.0
83786 Kidney Ca, Nuclear grade 2 (OD04338)	0.0	0.0
83787 Kidney NAT (OD04338)	0.2	0.2
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	0.0	0.0
83789 Kidney NAT (OD04339)	0.0	0.0
83790 Kidney Ca, Clear cell type (OD04340)	0.1	0.2
83791 Kidney NAT (OD04340)	0.0	0.2
83792 Kidney Ca, Nuclear grade 3 (OD04348)	0.0	0.0
83793 Kidney NAT (OD04348)	0.0	0.1
87474 Kidney Cancer (OD04622-01)	0.4	0.4
87475 Kidney NAT (OD04622-03)	0.0	0.0
85973 Kidney Cancer (OD04450-01)	0.0	0.0

85974 Kidney NAT (OD04450-03)	0.0	0.0
Kidney Cancer Clontech 8120607	0.4	0.3
Kidney NAT Clontech 8120608	0.0	0.0
Kidney Cancer Clontech 8120613	0.0	0.0
Kidney NAT Clontech 8120614	0.0	0.0
Kidney Cancer Clontech 9010320	0.0	0.0
Kidney NAT Clontech 9010321	0.0	0.0
Normal Uterus GENPAK 061018	0.1	0.0
Uterus Cancer GENPAK 064011	0.5	0.6
Normal Thyroid Clontech A+ 6570-1	0.5	0.4
Thyroid Cancer GENPAK 064010	0.0	0.0
Thyroid Cancer INVITROGEN A302152	0.0	0.0
Thyroid NAT INVITROGEN A302153	0.2	0.1
Normal Breast GENPAK 061019	5.5	5.6
84877 Breast Cancer (OD04566)	0.5	0.7
85975 Breast Cancer (OD04590-01)	3.0	3.9
85976 Breast Cancer Mets (OD04590-03)	1.4	1.7
87070 Breast Cancer Metastasis (OD04655-05)	100.0	100.0
GENPAK Breast Cancer 064006	1.7	2.0
Breast Cancer Res. Gen. 1024	0.8	0.8
Breast Cancer Clontech 9100266	3.5	4.1
Breast NAT Clontech 9100265	3.5	4.2
Breast Cancer INVITROGEN A209073	0.7	0.7
Breast NAT INVITROGEN A2090734	1.1	1.3
Normal Liver GENPAK 061009	2.0	1.7
Liver Cancer GENPAK 064003	0.0	0.0
Liver Cancer Research Genetics RNA 1025	0.3	0.3
Liver Cancer Research Genetics RNA 1026	0.0	0.0
Paired Liver Cancer Tissue Research Genetics RNA 6004-T	0.2	0.1
Paired Liver Tissue Research Genetics RNA 6004-N	0.0	0.1
Paired Liver Cancer Tissue Research Genetics RNA 6005-T	0.0	0.0
Paired Liver Tissue Research Genetics RNA 6005-N	0.1	0.1
Normal Bladder GENPAK 061001	0.2	0.1
Bladder Cancer Research Genetics RNA 1023	3.0	3.1
Bladder Cancer INVITROGEN A302173	1.0	0.8
87071 Bladder Cancer (OD04718-01)	0.0	0.0
87072 Bladder Normal Adjacent (OD04718-03)	4.1	3.4
Normal Ovary Res. Gen.	0.0	0.0
Ovarian Cancer GENPAK 064008	1.6	1.4
87492 Ovary Cancer (OD04768-07)	0.0	0.0
87493 Ovary NAT (OD04768-08)	0.0	0.0
Normal Stomach GENPAK 061017	1.0	1.7
Gastric Cancer Clontech 9060358	0.2	0.2
NAT Stomach Clontech 9060359	0.1	0.2
Gastric Cancer Clontech 9060395	0.4	0.7

NAT Stomach Clontech 9060394	0.4	0.4
Gastric Cancer Clontech 9060397	0.1	0.3
NAT Stomach Clontech 9060396	0.1	0.2
Gastric Cancer GENPAK 064005	1.0	1.3

Table 17. Panel 3D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	3dtm5226f_ag1094		3dtm5226f_ag1094
94905_Daoy_Medulloblastoma/Cerebellum_sscDNA	0.0	94954_Ca Ski_Cervical epidermoid carcinoma (metastasis) sscDNA	0.1
94906_TE671_Medulloblastoma/Cerebellum_sscDNA	0.2	94955_ES-2_Ovarian clear cell carcinoma sscDNA	0.0
94907_D283_Med_Medulloblastoma/Cerebellum_sscDNA	0.2	94957_Ramos/6h stim_ Stimulated with PMA/ionomycin 6h sscDNA	0.1
94908_PFSK-1_Primitive Neuroectodermal/Cerebellum_sscDNA	1.6	94958_Ramos/14h stim_ Stimulated with PMA/ionomycin 14h sscDNA	0.0
94909_XF-498_CNS_sscDNA	30.4	94962_MEQ-01_Chronic myelogenous leukemia (megakaryoblast) sscDNA	1.7
94910_SNBT-78 CNS/glioma sscDNA	0.7	94963_Raji_Burkitt's lymphoma sscDNA	0.0
94911_SF-268_CNS/glioblastoma_sscDNA	0.0	94964_Daudi_Burkitt's lymphoma sscDNA	0.0
94912_T98G_Glioblastoma_sscDNA	3.3	94965_U266_B-cell plasmacytoma/myeloma_sscDNA	0.2
96776_SK-N-SH_Neuroblastoma (metastasis) sscDNA	22.4	94968_CA46_Burkitt's lymphoma sscDNA	0.0
94913_SF-295_CNS/glioblastoma_sscDNA	27.2	94970_RL_non-Hodgkin's B-cell lymphoma sscDNA	0.1
94914 Cerebellum sscDNA	6.7	94972_JM1_pre-B-cell lymphoma/leukemia sscDNA	0.0
96777 Cerebellum sscDNA	0.0	94973_Jurkat_T cell leukemia sscDNA	0.0
94916_NCI-H292_Mucoepidermoid lung carcinoma sscDNA	21.9	94974_TF-1_Erythroleukemia sscDNA	2.1
94917_DMS-114_Small cell lung cancer sscDNA	2.4	94975_HUT 78_T-cell lymphoma sscDNA	0.0
94918_DMS-79_Small cell lung cancer/neuroendocrine sscDNA	0.0	94977_U937_Histiocytic lymphoma sscDNA	0.0

94919_NCI-H146_Small cell lung cancer/neuroendocrine sscDNA	100.0	94980_KU-812_Myelogenous leukemia sscDNA	8.2
94920_NCI-H526_Small cell lung cancer/neuroendocrine sscDNA	0.0	94981_769-P_Clear cell renal carcinoma sscDNA	0.0
94921_NCI-N417_Small cell lung cancer/neuroendocrine sscDNA	0.0	94983_Caki-2_Clear cell renal carcinoma sscDNA	0.3
94923_NCI-H82_Small cell lung cancer/neuroendocrine sscDNA	0.3	94984_SW 839_Clear cell renal carcinoma sscDNA	0.0
94924_NCI-H157_Squamous cell lung cancer (metastasis) sscDNA	0.0	94986_G401_Wilms' tumor sscDNA	0.0
94925_NCI-H1155_Large cell lung cancer/neuroendocrine sscDNA	65.1	94987_Hs766T_Pancreatic carcinoma (LN metastasis) sscDNA	4.9
94926_NCI-H1299_Large cell lung cancer/neuroendocrine sscDNA	0.0	94988_CAPAN-1_Pancreatic adenocarcinoma (liver metastasis) sscDNA	0.3
94927_NCI-H727_Lung carcinoid sscDNA	13.8	94989_SU86.86_Pancreatic carcinoma (liver metastasis) sscDNA	1.5
94928_NCI-UMC-11_Lung carcinoid sscDNA	28.7	94990_BxPC-3_Pancreatic adenocarcinoma sscDNA	23.7
94929_LX-1_Small cell lung cancer sscDNA	0.7	94991_HPAC_Pancreatic adenocarcinoma sscDNA	76.8
94930_Colo-205_Colon cancer sscDNA	0.0	94992_MIA PaCa-2_Pancreatic carcinoma sscDNA	0.5
94931_KM12_Colon cancer sscDNA	0.1	94993_CFPAC-1_Pancreatic ductal adenocarcinoma sscDNA	0.5
94932_KM20L2_Colon cancer sscDNA	7.3	94994_PANC-1_Pancreatic epithelioid ductal carcinoma sscDNA	6.9
94933_NCI-H716_Colon cancer sscDNA	80.1	94996_T24_Bladder carcinoma (transitional cell) sscDNA	4.1
94935_SW-48_Colon adenocarcinoma sscDNA	0.3	94997_5637_Bladder carcinoma sscDNA	1.0
94936_SW1116_Colon adenocarcinoma sscDNA	0.0	94998_HT-1197_Bladder carcinoma sscDNA	2.4
94937_LS 174T_Colon adenocarcinoma sscDNA	0.0	94999_UM-UC-3_Bladder carcinoma (transitional cell) sscDNA	0.0
94938_SW-948_Colon adenocarcinoma sscDNA	0.6	95000_A204_Rhabdomyosarcoma sscDNA	0.3
94939_SW-480_Colon adenocarcinoma sscDNA	0.0	95001_HT-1080_Fibrosarcoma sscDNA	0.2
94940_NCI-SNU-5_Gastric carcinoma sscDNA	0.0	95002_MG-63_Osteosarcoma (bone) sscDNA	0.2
94941_KATO III_Gastric carcinoma sscDNA	0.0	95003_SK-LMS-1_Leiomyosarcoma (vulva) sscDNA	0.0

94943_NCI-SNU-16_Gastric carcinoma sscDNA	1.7	95004_SJRH30_Rhabdomyosarcoma (met to bone marrow) sscDNA	0.2
94944_NCI-SNU-1_Gastric carcinoma sscDNA	0.0	95005_A431_Epidermoid carcinoma sscDNA	0.0
94946_RF-1_Gastric adenocarcinoma sscDNA	0.0	95007_WM266-4_Melanoma sscDNA	0.4
94947_RF-48_Gastric adenocarcinoma sscDNA	0.0	95010_DU 145_Prostate carcinoma (brain metastasis) sscDNA	0.0
96778_MKN-45_Gastric carcinoma sscDNA	0.1	95012_MDA-MB-468_Breast adenocarcinoma sscDNA	1.3
94949_NCI-N87_Gastric carcinoma sscDNA	2.4	95013_SCC-4_Squamous cell carcinoma of tongue sscDNA	0.2
94951_OVCAR-5_Ovarian carcinoma sscDNA	0.0	95014_SCC-9_Squamous cell carcinoma of tongue sscDNA	0.0
94952_RL95-2_Uterine carcinoma sscDNA	2.8	95015_SCC-15_Squamous cell carcinoma of tongue sscDNA	0.3
94953_HelaS3_Cervical adenocarcinoma sscDNA	0.2	95017_CAL 27_Squamous cell carcinoma of tongue sscDNA	1.6

Table 18. Panel 4D

Tissue Name	Relative Expression (%)	Tissue Name	Relative Expression (%)
	4Dtm2495f_ag1094		4Dtm2495f_ag1094
93768_Secondary Th1_anti-CD28/anti-CD3	0.0	93100_HUVEC (Endothelial)_IL-1b	0.0
93769_Secondary Th2_anti-CD28/anti-CD3	0.1	93779_HUVEC (Endothelial)_IFN gamma	0.0
93770_Secondary Tr1_anti-CD28/anti-CD3	0.0	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.0
93573_Secondary Th1_resting day 4-6 in IL-2	0.0	93101_HUVEC (Endothelial)_TNF alpha + IL4	0.3
93572_Secondary Th2_resting day 4-6 in IL-2	0.0	93781_HUVEC (Endothelial)_IL-11	0.0
93571_Secondary Tr1_resting day 4-6 in IL-2	0.0	93583_Lung Microvascular Endothelial Cells none	0.0
93568_primary Th1_anti-CD28/anti-CD3	0.0	93584_Lung Microvascular Endothelial Cells TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93569_primary Th2_anti-CD28/anti-CD3	0.0	92662_Microvascular Dermal endothelium none	0.0
93570_primary Tr1_anti-CD28/anti-CD3	0.0	92663_Microvasular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93565_primary Th1_resting dy 4-6 in IL-2	0.0	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	3.7

93566_primary Th2_resting dy 4-6 in IL-2	0.0	93347_Small Airway Epithelium none	4.5
93567_primary Tr1_resting dy 4-6 in IL-2	0.0	93348_Small Airway Epithelium_TNF α (4 ng/ml) and IL1b (1 ng/ml)	1.7
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	0.0	92668_Coronary Artery SMC resting	0.0
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	0.0	92669_Coronary Artery SMC_TNF α (4 ng/ml) and IL1b (1 ng/ml)	0.0
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.0	93107_astrocytes resting	8.5
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0.0	93108_astrocytes_TNF α (4 ng/ml) and IL1b (1 ng/ml)	0.2
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.3	92666_KU-812 (Basophil) resting	8.3
93354_CD4 none	0.0	92667_KU-812 (Basophil) PMA/ionoycin	100.0
93252_Secondary Th1/Th2/Tr1 anti-CD95 CH11	0.0	93579_CCD1106 (Keratinocytes) none	70.2
93103_LAK cells resting	0.0	93580_CCD1106 (Keratinocytes)_TNF α and IFNg **	3.0
93788_LAK cells IL-2	0.0	93791_Liver Cirrhosis	1.3
93787_LAK cells IL-2+IL-12	4.2	93792_Lupus Kidney	0.0
93789_LAK cells IL-2+IFN gamma	0.0	93577_NCI-H292	16.6
93790_LAK cells IL-2+IL-18	0.0	93358_NCI-H292 IL-4	10.4
93104_LAK cells_PMA/ionomycin and IL-18	0.0	93360_NCI-H292 IL-9	20.2
93578_NK Cells IL-2 resting	0.0	93359_NCI-H292 IL-13	6.3
93109_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93357_NCI-H292 IFN gamma	8.5
93110_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93777_HPAEC -	0.0
93111_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93778_HPAEC IL-1 beta/TNA alpha	0.0
93112_Mononuclear Cells (PBMCs) resting	0.0	93254_Normal Human Lung Fibroblast none	36.3
93113_Mononuclear Cells (PBMCs) PWM	0.0	93253_Normal Human Lung Fibroblast_TNF α (4 ng/ml) and IL-1b (1 ng/ml)	18.6
93114_Mononuclear Cells (PBMCs) PHA-L	0.0	93257_Normal Human Lung Fibroblast IL-4	16.0
93249_Ramos (B cell) none	0.0	93256_Normal Human Lung Fibroblast IL-9	4.4
93250_Ramos (B cell) ionomycin	0.3	93255_Normal Human Lung Fibroblast IL-13	11.4
93349_B lymphocytes PWM	0.0	93258_Normal Human Lung	36.9

		Fibroblast_IFN gamma	
93350_B lymphocytes_CD40L and IL-4	0.0	93106_Dermal Fibroblasts CCD1070 resting	0.1
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0.0	93361_Dermal Fibroblasts CCD1070 TNF alpha 4 ng/ml	0.0
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	0.0	93105_Dermal Fibroblasts CCD1070 IL-1 beta 1 ng/ml	0.0
93356_Dendritic Cells none	0.0	93772_dermal fibroblast IFN gamma	0.3
93355_Dendritic Cells_LPS 100 ng/ml	0.0	93771_dermal fibroblast IL-4	0.0
93775_Dendritic Cells_anti-CD40	0.0	93260 IBD Colitis 2	0.3
93774_Monocytes resting	0.0	93261 IBD Crohns	0.3
93776_Monocytes_LPS 50 ng/ml	0.0	735010 Colon normal	11.4
93581_Macrophages resting	41.8	735019 Lung none	5.3
93582_Macrophages_LPS 100 ng/ml	0.1	64028-1 Thymus none	1.2
93098_HUVEC (Endothelial) none	1.7	64030-1 Kidney none	2.0
93099_HUVEC (Endothelial) starved	0.0		

Panel 1 Summary: Ag273b Expression of the NOV1a gene is highest in a metastatic prostate cancer cell line PC-3 (CT = 26.8). There is also substantial expression of this gene in

5 a number of lung cancer cell lines and brain cancer cell lines. Thus, expression of the NOV1a gene could be used to distinguish lung, prostate or brain cancer cell lines from other samples. In addition, therapeutic inhibition of this gene product, through the use of small molecule drugs or antibodies, might have benefit in the treatment of lung, prostate or brain cancer. Among other normal tissues this gene is also low to moderately expressed in heart, colon, 10 small intestine, trachea, salivary gland, fetal liver, and mammary gland.

The NOV1a gene encodes a novel insulin-like growth factor binding protein acid labile subunit. Among CNS tissues, this gene is expressed at moderate levels in cerebellum and thalamus. Insulin-like growth factor (IGF) has been shown to have neuroprotective effects, as is currently under investigation as a biopharmaceutical for the treatment of amyotrophic lateral sclerosis. In serum, IGF is bound to both IGF-binding protein (IGFBP) and the acid labile subunit (IGFBP-ALS). In the brain, glia produce IGFBP; however the IGFBP-ALS has not been detected in the CNS. Therefore, the NOV1a gene may represent the CNS equivalent of IGFBP-ALS. Because of the neuroprotective effects of IGF, therapeutic modulation of this

gene or its protein product may be useful in treating diseases in which neuronal death/degeneration occur such as amyotrophic lateral sclerosis, multiple sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, spinocerebellar ataxia, or CNS injury such as stroke, head or spinal cord trauma.

5

Panel 1.3D Summary: Ag1094 Results from two experiments using the same probe/primer set are in excellent agreement and are consistent with what is observed in Panel 1. Expression of the NOV1a gene is highest in a lung cancer cell line (CT = 28). There is also substantial expression of this gene in a number of additional lung cancer cell lines and brain 10 cancer cell lines as well as in a metastatic prostate cancer cell line. Thus, NOV1a gene expression could be used to distinguish prostate, lung or brain cancer cell lines from other samples. In addition, therapeutic inhibition of this gene product, through the use of small molecule drugs or antibodies, might have benefit in the treatment of prostate, lung or brain cancer.

15

Among CNS tissues, there is low but significant expression in thalamus and cerebellum. Please see Panel 1 summary for description of potential utility of this gene in the CNS.

Panel 2D Summary: Ag1094 Results from two experiments using the same probe/primer set are in good agreement. Expression of the NOV1a gene is highest in a 20 metastatic breast cancer sample (CT = 26-27). In addition, several other breast cancer and lung cancer samples show increased expression when compared to their normal adjacent margin samples. This observation is consistent with the results in Panel 1.3D that show higher NOV1a gene expression in lung cancer cell lines. Thus, expression of this gene might be used 25 to distinguish breast cancer or lung cancer tissue from their normal counterparts and might be of diagnostic value. Moreover, therapeutic modulation of the NOV1a gene or its gene product, through the use of small molecule drugs or antibodies, may be of benefit for treatment of breast or lung cancer.

30

Panel 3D Summary: Ag1094 Expression of the NOV1a gene is highest in a small cell lung cancer cell line (CT = 28.5). In addition, there is significant expression of this gene in other lung cancer cell lines as well as in several brain cancer and pancreatic cancer cell lines. These results are consistent with what is observed in the other panels. Thus, the expression of the NOV1a gene may be used to distinguish lung, breast or pancreas cancer cell line samples 35 from other tissues. Moreover, therapeutic modulation of this gene or gene product, through

the use of small molecule drugs or antibodies, may be of benefit for treatment of lung, breast or pancreatic cancer.

Panel 4D Summary: Ag1094 The NOV1a gene is expressed at high levels in basophils
5 (CT 28.3) as well as in keratinocytes and normal lung fibroblasts (independently of their activation status). In addition, this gene is expressed at a lower level in a muco-epidermoid cell line (H292). Expression of the NOV1a gene is also found in normal lung which is consistent with the data from Panel 1.3D. The protein encoded by this transcript is a homolog of insulin-like growth factor binding protein acid labile subunit, a component of the systemic insulin-like
10 growth factor-binding protein (IGFBP) complex. Therefore, this gene may play an important role in the biology of circulating IGFs. IGFs are involved in a wide array of cellular processes such as proliferation, prevention of apoptosis, and differentiation. Thus, the NOV1a gene may be a suitable target for protein therapeutic to modulate locally the mitogenic effect of IGF and could be useful in the treatment of emphysema, COPD, or skin related disease.

15

References:

1. Mewar R., McMorris F.A. (1997) Expression of insulin-like growth factor-binding protein messenger RNAs in developing rat oligodendrocytes and astrocytes. J. Neurosci. Res 20 50:721-728.

Insulin-like growth factors, IGF-I and IGF-II, are potent regulators of oligodendrocyte development. Most of the IGF present in vivo is bound to members of a family of six high-affinity IGF-binding proteins (IGFBPs), which can either potentiate or inhibit IGF action, depending on other conditions. Additionally, serum contains a structurally unrelated protein,
25 acid-labile sub-unit (ALS), which forms a ternary complex with IGF and IGFBP3. In this study, reverse-transcriptase polymerase chain reaction (RT-PCR) was used to examine the expression of mRNAs for IGFBP 1-6 and ALS in purified populations of oligodendroglial cells and astrocytes. Astrocytes express all six IGFBPs. A2B5+/O4- oligodendrocyte precursors, O4+/O1- intermediate precursors, and O1+ oligodendrocytes express IGFBP3, 5,
30 and 6, while IGFBP4 is expressed in oligodendrocyte precursors but not at more mature stages. They were unable to detect ALS mRNA in whole brain or in cultured oligodendroglial cells. The presence of differentially expressed IGFBPs in developing oligodendrocytes and astrocytes could significantly affect the biological activity of IGF-I and IGF-II in the central nervous system and the IGF-responsiveness of the IGFBP-expressing cells.

35

PMID: 9418960

2. Arnold P.M., Ma J.Y., Citron B.A., Zoubine M.N., Festoff B.W. (2000) Selective developmental regulation of gene expression for insulin-like growth factor-binding proteins in
5 mouse spinal cord. Spine 25:1765-1770.

STUDY DESIGN: Prospective, randomized experimental study in mice. STUDY

OBJECTIVE: To determine whether insulin-like growth factor binding proteins (IGFBPs) are present in mouse spinal cord and, if so, what role they play in its development. SUMMARY

10 OF BACKGROUND DATA: Insulin-like growth factors are well recognized hormonal effectors of growth hormone and are expressed in the mammalian spinal cord. The IGFBPs are a group of six genetically distinct proteins that bind IGFs and modulate their bioactivity. They appear in the brain during development, localize to the neuromuscular junction, and promote motor neuron survival. The benefit of IGF-I in amyotrophic lateral sclerosis ALS and its
15 potential use in preventing motor neuron apoptosis in spinal cord injury dictates that studies of the presence and response of IGFBPs in that tissue be performed. METHODS: The IGFBPs in mouse spinal cord were analyzed by Western ligand blot, Western immunoblot, and reverse transcription-polymerase chain reaction at various time points from embryonic day 14 to postnatal day 30. RESULTS: Three IGFBPs with molecular masses of 24, 28, and 32 kDa
20 were found, the latter two being the most prominent. The data indicate that these are IGFBP-4, -5, and -2. CONCLUSION: Both IGFBP-2 and BP-5 are developmentally regulated in mouse spinal cord, with higher levels of those at early embryonic stages indicating their potential role in development of the mouse spinal cord.

25 PMID: 10888943

3. Corse A.M., Bilak M.M., Bilak S.R., Lehar M., Rothstein J.D., Kuncl R.W. (1999) Preclinical testing of neuroprotective neurotrophic factors in a model of chronic motor neuron degeneration. Neurobiol. Dis. 6:335-346.

30 Many neurotrophic factors have been shown to enhance survival of embryonic motor neurons or affect their response to injury. Few studies have investigated the potential effects of neurotrophic factors on more mature motor neurons that might be relevant for neurodegenerative diseases. Using organotypic spinal cord cultures from postnatal rats, researchers have demonstrated that insulin-like growth factor-I (IGF-I) and glial-derived

neurotrophic factor (GDNF) significantly increase choline acetyltransferase (ChAT) activity, but brain-derived neurotrophic factor (BDNF), neurotrophin-4 (NT-4/5), and neurotrophin-3 (NT-3) do not. Surprisingly, ciliary neurotrophic factor (CNTF) actually reduces ChAT activity compared to age-matched control cultures. Neurotrophic factors have also been shown
 5 to alter the sensitivity of some neurons to glutamate neurotoxicity, a postulated mechanism of injury in the neurodegenerative disease, amyotrophic lateral sclerosis (ALS). Incubation of organotypic spinal cord cultures in the presence of the glutamate transport inhibitor threo-hydroxyaspartate (THA) reproducibly causes death of motor neurons which is glutamate-mediated. In this model of motor neuron degeneration, IGF-I, GDNF, and NT-4/5 are potently
 10 neuroprotective, but BDNF, CNTF, and NT-3 are not. The organotypic glutamate toxicity model appears to be the best preclinical predictor to date of success in human clinical trials in ALS.

NOV3a

Expression of gene NOV3a was assessed using the primer-probe set Ag2100,
 15 described in Table 19. Results from RTQ-PCR runs are shown in Tables 20, 21, 22, 23, and 24.

Table 19. Probe Name Ag2100

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5' -AGATCCCTGGAACAGAGGATT-3'	59	21	2446	97
Probe	TET-5'- TGCTGAAGCCAATAAACTTGCAGCA- 3'-TAMRA	67.9	26	2474	98
Reverse	5' -CCTTCATGTTCCCTTGAA-3'	58.9	21	2513	99

20

Table 20. Panel 1.3D

Tissue Name	Relative Expression(%) 1.3dtm3300t_ag2100	Tissue Name	Relative Expression(%)
			1.3dtm3300t_ag2100
Liver adenocarcinoma	11.7	Kidney (fetal)	1.8
Pancreas	0.0	Renal ca. 786-0	7.1
Pancreatic ca. CAPAN 2	3.2	Renal ca. A498	3.7
Adrenal gland	1.4	Renal ca. RXF 393	3.1
Thyroid	0.1	Renal ca. ACHN	4.4
Salivary gland	0.1	Renal ca. UO-31	6.3
Pituitary gland	2.1	Renal ca. TK-10	3.2

Brain (fetal)	2.1	Liver	0.0
Brain (whole)	24.7	Liver (fetal)	3.8
Brain (amygdala)	11.2	Liver ca. (hepatoblast) HepG2	3.2
Brain (cerebellum)	2.7	Lung	0.3
Brain (hippocampus)	36.3	Lung (fetal)	0.9
Brain (substantia nigra)	1.5	Lung ca. (small cell) LX-1	6.6
Brain (thalamus)	30.4	Lung ca. (small cell) NCI-H69	8.5
Cerebral Cortex	100.0	Lung ca. (s.cell var.) SHP-77	7.5
Spinal cord	2.5	Lung ca. (large cell) NCI-H460	0.0
CNS ca. (glio/astro) U87-MG	6.4	Lung ca. (non-sm. cell) A549	0.2
CNS ca. (glio/astro) U-118-MG	33.7	Lung ca. (non-s.cell) NCI-H23	10.4
CNS ca. (astro) SW1783	5.9	Lung ca (non-s.cell) HOP-62	1.4
CNS ca.* (neuro; met) SK-N-AS	14.5	Lung ca. (non-s.cl) NCI-H522	5.3
CNS ca. (astro) SF-539	7.4	Lung ca. (squam.) SW 900	3.2
CNS ca. (astro) SNB-75	5.8	Lung ca. (squam.) NCI-H596	7.2
CNS ca. (glio) SNB-19	1.0	Mammary gland	0.2
CNS ca. (glio) U251	2.4	Breast ca.* (pl. effusion) MCF-7	5.6
CNS ca. (glio) SF-295	0.9	Breast ca.* (pl.ef) MDA-MB-231	14.5
Heart (fetal)	0.4	Breast ca.* (pl. effusion) T47D	2.4
Heart	0.1	Breast ca. BT-549	6.8
Fetal Skeletal	3.4	Breast ca. MDA-N	14.0
Skeletal muscle	0.0	Ovary	2.2
Bone marrow	5.4	Ovarian ca. OVCAR-3	2.5
Thymus	2.1	Ovarian ca. OVCAR-4	0.8
Spleen	0.6	Ovarian ca. OVCAR-5	2.7
Lymph node	0.4	Ovarian ca. OVCAR-8	3.2
Colorectal	1.8	Ovarian ca. IGROV-1	2.0
Stomach	1.0	Ovarian ca.* (ascites) SK-OV-3	7.4
Small intestine	1.6	Uterus	0.0
Colon ca. SW480	13.1	Placenta	0.2
Colon ca.* (SW480 met) SW620	4.5	Prostate	0.2
Colon ca. HT29	4.1	Prostate ca.* (bone met) PC-3	2.0
Colon ca. HCT-116	5.0	Testis	4.0
Colon ca. CaCo-2	5.9	Melanoma Hs688(A).T	0.7
83219 CC Well to Mod Diff (ODO3866)	2.8	Melanoma* (met) Hs688(B).T	0.3
Colon ca. HCC-2998	3.7	Melanoma UACC-62	0.5
Gastric ca.* (liver met) NCI-N87	2.3	Melanoma M14	7.2
Bladder	0.9	Melanoma LOX IMVI	2.8
Trachea	0.7	Melanoma* (met) SK-MEL-5	5.8
Kidney	0.7	Adipose	0.2

Table 21. Panel 2.2

Tissue Name	Relative Expression(%) 2.2x4tm6379t ag2100 b2	Tissue Name	Relative Expression(%) 2.2x4tm6379t ag2100 b2
Normal Colon GENPAK 061003	6.2	83793 Kidney NAT (OD04348)	30.3
97759 Colon cancer (OD06064)	13.4	98938 Kidney malignant cancer (OD06204B)	3.6
97760 Colon cancer NAT (OD06064)	9.0	98939 Kidney normal adjacent tissue (OD06204E)	10.5
97778 Colon cancer (OD06159)	4.5	85973 Kidney Cancer (OD04450-01)	2.4
97779 Colon cancer NAT (OD06159)	5.9	85974 Kidney NAT (OD04450-03)	13.3
98861 Colon cancer (OD06297-04)	3.8	Kidney Cancer Clontech 8120613	6.6
98862 Colon cancer NAT (OD06297-015)	10.0	Kidney NAT Clontech 8120614	1.2
83237 CC Gr.2 ascend colon (ODO3921)	4.3	Kidney Cancer Clontech 9010320	1.6
83238 CC NAT (ODO3921)	2.8	Kidney NAT Clontech 9010321	4.5
97766 Colon cancer metastasis (OD06104)	1.7	Kidney Cancer Clontech 8120607	0.5
97767 Lung NAT (OD06104)	3.1	Kidney NAT Clontech 8120608	1.7
87472 Colon mets to lung (OD04451-01)	9.6	Normal Uterus GENPAK 061018	1.1
87473 Lung NAT (OD04451-02)	3.2	Uterus Cancer GENPAK 064011	1.5
Normal Prostate Clontech A+ 6546-1 (8090438)	1.2	Normal Thyroid Clontech A+ 6570-1 (7080817)	0.0
84140 Prostate Cancer (OD04410)	0.0	Thyroid Cancer GENPAK 064010	0.6
84141 Prostate NAT (OD04410)	0.7	Thyroid Cancer INVITROGEN A302152	5.3
Normal Ovary Res. Gen.	2.8	Thyroid NAT INVITROGEN A302153	0.0
98863 Ovarian cancer (OD06283-03)	11.7	Normal Breast GENPAK 061019	3.0
98865 Ovarian cancer NAT/fallopian tube (OD06283-07)	3.0	84877 Breast Cancer (OD04566)	8.1
Ovarian Cancer GENPAK 064008	1.1	Breast Cancer Res. Gen. 1024	2.9
97773 Ovarian cancer (OD06145)	0.9	85975 Breast Cancer (OD04590-01)	14.7
97775 Ovarian cancer NAT (OD06145)	0.0	85976 Breast Cancer Mets (OD04590-03)	3.2
98853 Ovarian cancer (OD06455-03)	15.8	87070 Breast Cancer Metastasis (OD04655-05)	5.4
98854 Ovarian NAT (OD06455-07) Fallopian tube	1.8	GENPAK Breast Cancer 064006	3.1

Normal Lung GENPAK 061010	1.2	Breast Cancer Clontech 9100266	2.6
92337 Invasive poor diff. lung adeno (ODO4945-01)	8.4	Breast NAT Clontech 9100265	2.3
92338 Lung NAT (ODO4945-03)	1.2	Breast Cancer INVITROGEN A209073	1.8
84136 Lung Malignant Cancer (OD03126)	5.0	Breast NAT INVITROGEN A2090734	2.5
84137 Lung NAT (OD03126)	0.6	97763 Breast cancer (OD06083)	17.1
90372 Lung Cancer (OD05014A)	10.1	97764 Breast cancer node metastasis (OD06083)	14.6
90373 Lung NAT (OD05014B)	9.0	Normal Liver GENPAK 061009	0.4
97761 Lung cancer (OD06081)	10.1	Liver Cancer Research Genetics RNA 1026	0.0
97762 Lung cancer NAT (OD06081)	4.0	Liver Cancer Research Genetics RNA 1025	1.8
85950 Lung Cancer (OD04237-01)	4.1	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	1.1
85970 Lung NAT (OD04237-02)	2.0	Paired Liver Tissue Research Genetics RNA 6004-N	2.5
83255 Ocular Mel Met to Liver (ODO4310)	0.9	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	1.6
83256 Liver NAT (ODO4310)	0.4	Paired Liver Tissue Research Genetics RNA 6005-N	0.0
84139 Melanoma Mets to Lung (OD04321)	10.4	Liver Cancer GENPAK 064003	0.7
84138 Lung NAT (OD04321)	2.0	Normal Bladder GENPAK 061001	2.9
Normal Kidney GENPAK 061008	5.0	Bladder Cancer Research Genetics RNA 1023	1.5
83786 Kidney Ca, Nuclear grade 2 (OD04338)	15.3	Bladder Cancer INVITROGEN A302173	17.8
83787 Kidney NAT (OD04338)	5.1	Normal Stomach GENPAK 061017	10.4
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	100.0	Gastric Cancer Clontech 9060397	1.1
83789 Kidney NAT (OD04339)	9.3	NAT Stomach Clontech 9060396	0.7
83790 Kidney Ca, Clear cell type (OD04340)	14.0	Gastric Cancer Clontech 9060395	2.8
83791 Kidney NAT (OD04340)	11.2	NAT Stomach Clontech 9060394	2.8
83792 Kidney Ca, Nuclear grade 3 (OD04348)	9.0	Gastric Cancer GENPAK 064005	6.0

Table 22. Panel 3D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	3dx4tm5110t ag2100_a2		3dx4tm5110t ag2100_a2
94905_Daoy_Medulloblastoma/Cerebellum sscDNA	7.3	94954_Ca Ski_Cervical epidermoid carcinoma (metastasis) sscDNA	21.0
94906_TE671_Medulloblastoma/Cerebellum sscDNA	3.8	94955_ES-2_Ovarian clear cell carcinoma sscDNA	11.7
94907_D283_Med_Medulloblastoma/Cerebellum sscDNA	15.7	94957_Ramos/6h stim_ Stimulated with PMA/ionomycin 6h sscDNA	10.8
94908_PFSK-1_Primitive Neuroectodermal/Cerebellum_s scDNA	11.2	94958_Ramos/14h stim_ Stimulated with PMA/ionomycin 14h sscDNA	6.2
94909_XF-498_CNS(sscDNA)	21.2	94962_MEQ-01_Chronic myelogenous leukemia (megakaryoblast) sscDNA	5.8
94910_SNBT-78_CNS/glioma sscDNA	11.3	94963_Raji_Burkitt's lymphoma sscDNA	6.8
94911_SF-268_CNS/glioblastoma_sscDNA	7.6	94964_Daudi_Burkitt's lymphoma sscDNA	14.7
94912_T98G_Glioblastoma_sscDNA	12.0	94965_U266_B-cell plasmacytoma/myeloma_sscDNA	5.1
96776_SK-N-SH_Neuroblastoma (metastasis) sscDNA	5.6	94968_CA46_Burkitt's lymphoma sscDNA	5.0
94913_SF-295_CNS/glioblastoma_sscDNA	12.4	94970_RL_non-Hodgkin's B-cell lymphoma sscDNA	3.8
94914_Cerebellum sscDNA	16.1	94972_JM1_pre-B-cell lymphoma/leukemia sscDNA	11.5
96777_Cerebellum sscDNA	3.6	94973_Jurkat_T cell leukemia sscDNA	12.5
94916_NCI-H292_Mucoepidermoid lung carcinoma sscDNA	14.0	94974_TF-1_Erythroleukemia sscDNA	9.9
94917_DMS-114_Small cell lung cancer sscDNA	10.3	94975_HUT 78_T-cell lymphoma sscDNA	14.7
94918_DMS-79_Small cell lung cancer/neuroendocrine sscDNA	100.0	94977_U937_Histiocytic lymphoma sscDNA	8.1
94919_NCI-H146_Small cell lung cancer/neuroendocrine sscDNA	14.2	94980_KU-812_Myelogenous leukemia sscDNA	17.7
94920_NCI-H526_Small cell lung cancer/neuroendocrine sscDNA	19.8	94981_769-P_Clear cell renal carcinoma sscDNA	6.3
94921_NCI-N417_Small cell lung	5.7	94983_Caki-2_Clear cell renal carcinoma sscDNA	9.5

cancer/neuroendocrine_sscDNA			
94923_NCI-H82_Small cell lung cancer/neuroendocrine_sscDNA	10.1	94984_SW 839_Clear cell renal carcinoma sscDNA	5.2
94924_NCI-H157_Squamous cell lung cancer (metastasis) sscDNA	13.8	94986_G401_Wilms' tumor sscDNA	6.3
94925_NCI-H1155_Large cell lung cancer/neuroendocrine_sscDNA	36.0	94987_Hs766T_Pancreatic carcinoma (LN metastasis) sscDNA	15.7
94926_NCI-H1299_Large cell lung cancer/neuroendocrine_sscDNA	22.7	94988_CAPAN-1_Pancreatic adenocarcinoma (liver metastasis) sscDNA	8.6
94927_NCI-H727_Lung carcinoid sscDNA	14.3	94989_SU86.86_Pancreatic carcinoma (liver metastasis) sscDNA	14.0
94928_NCI-UMC-11_Lung carcinoid sscDNA	25.8	94990_BxPC-3_Pancreatic adenocarcinoma sscDNA	9.4
94929_LX-1_Small cell lung cancer sscDNA	11.0	94991_HPAC_Pancreatic adenocarcinoma sscDNA	14.4
94930_Colo-205_Colon cancer sscDNA	12.7	94992_MIA PaCa-2_Pancreatic carcinoma sscDNA	2.6
94931_KM12_Colon cancer sscDNA	17.1	94993_CFPAC-1_Pancreatic ductal adenocarcinoma sscDNA	38.5
94932_KM20L2_Colon cancer sscDNA	7.0	94994_PANC-1_Pancreatic epithelioid ductal carcinoma sscDNA	19.5
94933_NCI-H716_Colon cancer sscDNA	19.4	94996_T24_Bladder carcinoma (transitional cell) sscDNA	9.0
94935_SW-48_Colon adenocarcinoma sscDNA	10.6	94997_5637_Bladder carcinoma sscDNA	10.5
94936_SW1116_Colon adenocarcinoma sscDNA	7.7	94998_HT-1197_Bladder carcinoma sscDNA	4.8
94937_LS 174T_Colon adenocarcinoma sscDNA	9.8	94999_UM-UC-3_Bladder carcinoma (transitional cell) sscDNA	13.3
94938_SW-948_Colon adenocarcinoma sscDNA	1.4	95000_A204_Rhabdomyosarcoma sscDNA	15.2
94939_SW-480_Colon adenocarcinoma sscDNA	7.6	95001_HT-1080_Fibrosarcoma sscDNA	11.9
94940_NCI-SNU-5_Gastric carcinoma sscDNA	14.8	95002_MG-63_Osteosarcoma (bone) sscDNA	7.3
94941_KATO III_Gastric carcinoma sscDNA	18.8	95003_SK-LMS-1_Leiomyosarcoma (vulva) sscDNA	47.8
94943_NCI-SNU-16_Gastric carcinoma sscDNA	12.5	95004_SJRH30_Rhabdomyosarcoma (met to bone marrow) sscDNA	10.2
94944_NCI-SNU-1_Gastric carcinoma sscDNA	12.3	95005_A431_Epidermoid carcinoma sscDNA	12.1
94946_RF-1_Gastric adenocarcinoma sscDNA	5.3	95007_WM266-4_Melanoma sscDNA	21.8

94947_RF-48_Gastric adenocarcinoma sscDNA	7.7	95010_DU 145_Prostate carcinoma (brain metastasis) sscDNA	0.2
96778_MKN-45_Gastric carcinoma sscDNA	11.7	95012_MDA-MB-468_Breast adenocarcinoma sscDNA	5.6
94949_NCI-N87_Gastric carcinoma sscDNA	9.3	95013_SCC-4_Squamous cell carcinoma of tongue sscDNA	0.3
94951_OVCAR-5_Ovarian carcinoma sscDNA	3.0	95014_SCC-9_Squamous cell carcinoma of tongue sscDNA	0.3
94952_RL95-2_Uterine carcinoma sscDNA	4.5	95015_SCC-15_Squamous cell carcinoma of tongue sscDNA	0.2
94953_HelaS3_Cervical adenocarcinoma sscDNA	9.0	95017_CAL 27_Squamous cell carcinoma of tongue sscDNA	19.8

Table 23. Panel 4D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	4dtm3359t_ag2100		4dtm3359t_ag2100
93768_Secondary Th1_anti-CD28/anti-CD3	15.4	93100_HUVEC (Endothelial)_IL-1b	12.2
93769_Secondary Th2_anti-CD28/anti-CD3	11.9	93779_HUVEC (Endothelial)_IFN gamma	16.6
93770_Secondary Tr1_anti-CD28/anti-CD3	15.6	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	11.8
93573_Secondary Th1_resting day 4-6 in IL-2	4.9	93101_HUVEC (Endothelial)_TNF alpha + IL4	11.4
93572_Secondary Th2_resting day 4-6 in IL-2	3.3	93781_HUVEC (Endothelial)_IL-11	8.2
93571_Secondary Tr1_resting day 4-6 in IL-2	6.0	93583_Lung Microvascular Endothelial Cells none	7.3
93568_primary Th1_anti-CD28/anti-CD3	13.6	93584_Lung Microvascular Endothelial Cells_TNF α (4 ng/ml) and IL1b (1 ng/ml)	6.2
93569_primary Th2_anti-CD28/anti-CD3	12.0	92662_Microvascular Dermal endothelium none	23.3
93570_primary Tr1_anti-CD28/anti-CD3	22.2	92663_Microvascular Dermal endothelium_TNF α (4 ng/ml) and IL1b (1 ng/ml)	10.5
93565_primary Th1_resting dy 4-6 in IL-2	100.0	93773_Bronchial epithelium_TNF α (4 ng/ml) and IL1b (1 ng/ml) **	0.6
93566_primary Th2_resting dy 4-6 in IL-2	37.9	93347_Small Airway Epithelium none	1.6
93567_primary Tr1_resting dy 4-6 in IL-2	29.3	93348_Small Airway Epithelium_TNF α (4 ng/ml) and IL1b (1 ng/ml)	7.4
93351_CD45RA CD4 lymphocyte anti-CD28/anti-CD3	13.6	92668_Coronery Artery SMC resting	4.4

93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	15.4	92669_Coronery Artery SMC_TNF α (4 ng/ml) and IL1b (1 ng/ml)	2.0
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	10.6	93107_astrocytes_resting	1.3
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	7.9	93108_astrocytes_TNF α (4 ng/ml) and IL1b (1 ng/ml)	0.5
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	17.3	92666_KU-812 (Basophil)_resting	22.4
93354_CD4 none	0.5	92667_KU-812 (Basophil) PMA/ionoycin	28.5
93252_Secondary Th1/Tb2/Tr1 anti-CD95 CH11	17.1	93579_CCD1106 (Keratinocytes) none	14.3
93103_LAK cells resting	3.6	93580_CCD1106 (Keratinocytes)_TNF α and IFNg **	18.4
93788_LAK cells IL-2	16.8	93791_Liver Cirrhosis	0.5
93787_LAK cells IL-2+IL-12	8.4	93792_Lupus Kidney	3.3
93789_LAK cells IL-2+IFN gamma	16.4	93577_NCI-H292	29.5
93790_LAK cells IL-2+ IL-18	16.8	93358_NCI-H292 IL-4	27.7
93104_LAK cells_PMA/ionomycin and IL-18	0.6	93360_NCI-H292 IL-9	32.3
93578_NK Cells IL-2 resting	15.3	93359_NCI-H292 IL-13	13.4
93109_Mixed Lymphocyte Reaction Two Way MLR	1.8	93357_NCI-H292 IFN gamma	11.0
93110_Mixed Lymphocyte Reaction Two Way MLR	6.1	93777_HPAEC -	8.5
93111_Mixed Lymphocyte Reaction Two Way MLR	10.1	93778_HPAEC IL-1 beta/TNA alpha	7.7
93112_Mononuclear Cells (PBMCs) resting	0.1	93254_Normal Human Lung Fibroblast none	6.3
93113_Mononuclear Cells (PBMCs) PWM	25.5	93253_Normal Human Lung Fibroblast_TNF α (4 ng/ml) and IL-1b (1 ng/ml)	9.0
93114_Mononuclear Cells (PBMCs) PHA-L	24.0	93257_Normal Human Lung Fibroblast IL-4	3.7
93249_Ramos (B cell) none	17.7	93256_Normal Human Lung Fibroblast IL-9	5.0
93250_Ramos (B cell) ionomycin	92.0	93255_Normal Human Lung Fibroblast IL-13	1.7
93349_B lymphocytes PWM	48.6	93258_Normal Human Lung Fibroblast IFN gamma	3.4
93350_B lymphocytes_CD40L and IL-4	16.4	93106_Dermal Fibroblasts CCD1070_resting	57.4
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	10.5	93361_Dermal Fibroblasts CCD1070 TNF alpha 4 ng/ml	79.0
93248_EOL-1 (Eosinophil) dbcAMP/PMAion	7.0	93105_Dermal Fibroblasts CCD1070 IL-1 beta 1 ng/ml	21.8

omycin			
93356 Dendritic Cells none	0.5	93772_dermal fibroblast IFN gamma	22.2
93355_Dendritic Cells_LPS 100 ng/ml	0.0	93771_dermal fibroblast IL-4	45.7
93775_Dendritic Cells_anti-CD40	0.0	93260 IBD Colitis 2	0.9
93774_Monocytes resting	0.2	93261 IBD Crohns	1.0
93776_Monocytes_LPS 50 ng/ml	0.0	735010 Colon normal	3.7
93581_Macrophages resting	4.4	735019 Lung none	1.5
93582_Macrophages_LPS 100 ng/ml	0.6	64028-1 Thymus none	13.0
93098_HUVEC (Endothelial) none	24.7	64030-1 Kidney none	31.2
93099_HUVEC (Endothelial) starved	43.5		

Table 24. AI_comprehensive_panel_v1.0

Tissue Name	Relative Expression(%)	
	tm7130t_ag2100_a2	tm7159t_ag2100_b1
110967 COPD-F	0.5	0.8
110980 COPD-F	1.5	1.2
110968 COPD-M	0.4	0.6
110977 COPD-M	1.5	1.9
110989 Emphysema-F	4.2	6.0
110992 Emphysema-F	2.8	2.9
110993 Emphysema-F	0.9	0.8
110994 Emphysema-F	0.7	0.4
110995 Emphysema-F	2.0	5.4
110996 Emphysema-F	2.2	2.4
110997 Asthma-M	1.9	3.1
111001 Asthma-F	1.4	2.7
111002 Asthma-F	1.0	1.0
111003 Atopic Asthma-F	4.0	2.2
111004 Atopic Asthma-F	16.6	17.0
111005 Atopic Asthma-F	7.2	5.5
111006 Atopic Asthma-F	0.9	0.7
111417 Allergy-M	1.9	2.4
112347 Allergy-M	0.0	0.0
112349 Normal Lung-F	0.0	0.0
112357 Normal Lung-F	6.1	6.0
112354 Normal Lung-M	1.5	2.3
112374 Crohns-F	2.9	5.2

112389 Match Control Crohns-F	9.0	6.8
112375 Crohns-F	2.5	3.8
112732 Match Control Crohns-F	3.8	5.4
112725 Crohns-M	0.1	0.7
112387 Match Control Crohns-M	1.0	1.4
112378 Crohns-M	0.0	0.0
112390 Match Control Crohns-M	2.5	1.8
112726 Crohns-M	3.8	5.9
112731 Match Control Crohns-M	3.6	6.7
112380 Ulcer Col-F	4.9	4.9
112734 Match Control Ulcer Col-F	12.6	12.0
112384 Ulcer Col-F	6.6	10.2
112737 Match Control Ulcer Col-F	4.1	6.1
112386 Ulcer Col-F	0.5	1.2
112738 Match Control Ulcer Col-F	7.5	7.9
112381 Ulcer Col-M	0.1	0.0
112735 Match Control Ulcer Col-M	2.9	2.3
112382 Ulcer Col-M	6.8	8.4
112394 Match Control Ulcer Col-M	0.5	0.5
112383 Ulcer Col-M	12.1	14.6
112736 Match Control Ulcer Col-M	3.5	5.3
112423 Psoriasis-F	1.4	1.1
112427 Match Control Psoriasis-F	2.9	1.8
112418 Psoriasis-M	0.8	0.8
112723 Match Control Psoriasis-M	6.1	7.4
112419 Psoriasis-M	1.0	1.3
112424 Match Control Psoriasis-M	0.4	1.2
112420 Psoriasis-M	1.8	2.4
112425 Match Control Psoriasis-M	2.2	2.7
104689 (MF) OA Bone-Backus	12.1	13.2
104690 (MF) Adj "Normal" Bone-Backus	5.4	4.2
104691 (MF) OA Synovium-Backus	43.3	35.7
104692 (BA) OA Cartilage-Backus	0.9	0.4
104694 (BA) OA Bone-Backus	16.8	16.7
104695 (BA) Adj "Normal" Bone-Backus	6.5	6.1
104696 (BA) OA Synovium-Backus	24.0	24.2
104700 (SS) OA Bone-Backus	12.3	35.1
104701 (SS) Adj "Normal" Bone-Backus	7.9	9.5
104702 (SS) OA Synovium-Backus	8.3	7.9
117093 OA Cartilage Rep7	2.0	2.3
112672 OA Bone5	1.9	0.8
112673 OA Synovium5	0.3	1.2
112674 OA Synovial Fluid cells5	0.5	0.4
117100 OA Cartilage Rep14	0.4	0.3
112756 OA Bone9	100.0	100.0

112757 OA Synovium9	0.5	0.2
112758 OA Synovial Fluid Cells9	0.8	1.5
117125 RA Cartilage Rep2	1.0	0.6
113492 Bone2 RA	2.8	3.6
113493 Synovium2 RA	1.7	0.7
113494 Syn Fluid Cells RA	0.9	2.1
113499 Cartilage4 RA	2.1	1.8
113500 Bone4 RA	1.8	2.5
113501 Synovium4 RA	2.1	2.3
113502 Syn Fluid Cells4 RA	1.0	0.8
113495 Cartilage3 RA	2.5	2.6
113496 Bone3 RA	2.0	2.1
113497 Synovium3 RA	1.3	1.4
113498 Syn Fluid Cells3 RA	2.9	3.2
117106 Normal Cartilage Rep20	0.1	0.7
113663 Bone3 Normal	0.3	0.1
113664 Synovium3 Normal	0.0	0.0
113665 Syn Fluid Cells3 Normal	0.1	0.2
117107 Normal Cartilage Rep22	0.9	0.3
113667 Bone4 Normal	0.4	0.7
113668 Synovium4 Normal	1.0	1.1
113669 Syn Fluid Cells4 Normal	1.0	0.7

Panel 1.3D Summary: Ag2100 Expression of the NOV3a gene is highest in cerebral cortex (CT = 26.3). This gene is expressed at more moderate levels in other parts of the CNS including amygdala, cerebellum, hippocampus, substantia nigra, thalamus, spinal cord, and fetal brain. Expression of the NOV3a gene in other normal tissues was lower than that in brain, suggesting a specific function for this protein in the CNS. Thus, this gene may be useful as a marker to distinguish brain from other tissues. The NOV3a gene encodes a protein with homology to citron-kinase. Citron-kinase (Citron-K) has been proposed by *in vitro* studies to be a crucial effector of Rho in regulation of cytokinesis. Citron-K is essential for cytokinesis in vivo in specific neuronal precursors and may play a fundamental role in specific human malformative syndromes of the CNS. General inhibitors of the RHO/RAC-INTERACTING CITRON KINASE family disrupt endothelial tight junctions, suggesting that specific modulators of this brain-preferential family member could be useful in delivery of therapeutics across the blood brain barrier. These general inhibitors also influence intracellular calcium flux, which is a central component of many important neuronal processes, such as apoptosis, neurotransmitter release and signal transduction. Thus, modulators of NOV3a protein function may prove useful in the treatment of neurodegenerative disorders involving apoptosis, such as

spinal muscular atrophy, Alzheimer's disease, Huntington's disease, Parkinson's disease, and others. Diseases involving neurotransmitters or signal transduction, such as schizophrenia, mania, stroke, epilepsy and depression may also benefit from agents that modulate the function of the NOV3a gene product.

5 The NOV3a gene also shows low expression in several metabolic tissues including adrenal gland (CT = 32), pituitary gland (CT = 32) and fetal heart (CT = 34). Interestingly, this gene is expressed at higher levels in adult skeletal muscle (CT = 37) compared to fetal skeletal muscle (CT = 31) as well as in adult liver (CT = 40) compared to fetal liver (CT = 31). Thus, the NOV3A gene may be used to differentiate between the fetal and adult skeletal muscle and
10 liver. Moreover, the therapeutic modulation of this gene, specifically its use in replacement type therapy through the administration of purified protein, might be beneficial in the treatment of diseases involving the degeneration of liver or skeletal muscle, such as muscular dystrophy.

15 **Panel 2.2 Summary:** Ag2100 Expression of the NOV3a gene is highest in a kidney cancer sample (CT = 28). In addition, there are a number of normal tissue/cancer tissue pairs in which this gene is expressed at higher levels in the tumor than the normal matched tissue. Thus, expression of the NOV3a gene could be used to distinguish between cancerous tissue and normal tissue. In addition, therapeutic modulation of this gene product, through the use of
20 small molecule drugs or antibodies, might be of benefit in the treatment of cancer.

25 **Panel 3D Summary:** Ag2100 Expression of the NOV3a gene is highest in a lung cancer cell line (CT = 26). However, low to moderate expression is also seen in the majority of cancer cell lines on this panel, suggesting that this gene may play an important role in many cell types.

30 **Panel 4D Summary:** Ag2100 The NOV3a gene is highly induced in Ramos B cells treated with PMA and ionomycin, in non-transformed B cells treated with PWM and in PBMC treated with PWM. All three of these observations are consistent with this transcript being induced in B cells after activation. Upon activation, T cells also produce this transcript, PBMC treated with PHA (T cell mitogen) express the transcript as well as primary activated Th1 cells. Primary Tr1 and Th2 express the transcript to a lesser extent. Fibroblast and endothelial cell lines on this panel also express NOV3a gene, although at lower levels as compared to the activated lymphocytes.

Role in inflammation: The NOV3a gene product has homology to the RHO/RAC-interacting citron kinase. The citron kinase may play an important role in T cell activation, by regulating TCR-mediated T cell spreading, chemotaxis and other chemokine responses and in apoptosis. Since the protein encoded for by the NOV3a gene has high homology to this kinase, 5 it too could contribute to T cell motility, activation and apoptosis. Likewise, this putative kinase may also be important in B cell motility, antigen receptor mediated activation and apoptosis.

Therapeutic function: Small molecule therapeutics designed against the protein encoded for by the NOV3a gene could reduce or inhibit inflammation. Anti-sense 10 therapeutics that would block the translation of the transcript and protein production could also inhibit inflammatory processes. These types of therapeutics could be important in the treatment of diseases such as osteoarthritis. Likewise, these therapeutics could be important in the treatment of asthma, psoriasis, diabetes, and IBD, which require activated T cells, as well as diseases that involve B cell activation such as systemic lupus erythematosus.

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AI_comprehensive_panel_v1.0 Summary: Ag2100 The NOV3A gene is highly expressed in bone isolated from 5 different osteoarthritic (OA) patients, synovium in 3 out of 5 OA patients, but not in cartilage from OA patients nor in any tissues from rheumatoid arthritis (RA) patients or in control samples. Thus, small molecule therapeutics designed against the 20 protein encoded for by the NOV3a gene could reduce or inhibit inflammation. Anti-sense therapeutics that would block the translation of the transcript and protein production could also inhibit inflammatory processes. These types of therapeutics could be important in the treatment of diseases such as osteoarthritis

25

References:

1. Di Cunto F., Imarisio S., Hirsch E., Broccoli V., Bulfone A., Miglieli A., Atzori C., Turco E., Triolo R., Dotto G.P., Silengo L., Altruda F. (2000) Defective neurogenesis in citron kinase knockout mice by altered cytokinesis and massive apoptosis. *Neuron* 28:115-127.
- 30 Citron-kinase (Citron-K) has been proposed by in vitro studies as a crucial effector of Rho in regulation of cytokinesis. To further investigate in vivo its biologic functions, we have inactivated Citron-K gene in mice by homologous recombination. Citron-K-/- mice grow at slower rates, are severely ataxic, and die before adulthood as a consequence of fatal seizures. Their brains display defective neurogenesis, with depletion of specific neuronal populations.
- 35 These abnormalities arise during development of the central nervous system due to altered

cytokinesis and massive apoptosis. The results indicate that Citron-K is essential for cytokinesis in vivo but only in specific neuronal precursors. Moreover, they suggest a novel molecular mechanism for a subset of human malformative syndromes of the CNS.

5 PMID: 11086988

2. Jezior J.R., Brady J.D., Rosenstein D.I., McCammon K.A., Miner A.S., Ratz P.H. (2001)

Dependency of detrusor contractions on calcium sensitization and calcium entry through LOE-
10 908-sensitive channels. Br. J. Pharmacol. 134:78-87.

The subcellular mechanisms regulating stimulus-contraction coupling in detrusor remain to be determined. Ca(2+)-free solutions, Ca(2+) channel blockers, cyclopiazonic acid (CPA), and RhoA kinase (ROK) inhibitors were used to test the hypothesis that Ca(2+) influx
15 and Ca(2+) sensitization play primary roles. In rabbit detrusor, peak bethanechol (BE)-induced force was inhibited 90% by incubation for 3 min in a Ca(2+)-free solution. By comparison, a 20 min incubation of rabbit femoral artery in a Ca(2+)-free solution reduced receptor-induced force by only 5%. In detrusor, inhibition of sarcoplasmic reticular (SR) Ca(2+) release by 2APB, or depletion of SR Ca(2+) by CPA, inhibited BE-induced force by only 27%. The
20 CPA-insensitive force was abolished by LaCl(3). By comparison, 2APB inhibited receptor-induced force in rabbit femoral artery by 71%. In the presence of the non-selective cation channel (NSCC) inhibitor, LOE-908, BE did not produce an increase in [Ca(2+)](i) but did produce weak increases in myosin phosphorylation and force. Inhibitors of ROK-induced
Ca(2+) sensitization, HA-1077 and Y-27632, inhibited BE-induced force by approximately
25 50%, and in combination with LOE-908, nearly abolished force. These data suggest that two principal muscarinic receptor-stimulated detrusor contractile mechanisms include NSCC activation, that elevates [Ca(2+)](i) and ROK activation, that sensitizes cross bridges to Ca(2+).

30 PMID: 11522599

3. Walsh S.V., Hopkins A.M., Chen J., Narumiya S., Parkos C.A., Nusrat A. (2001)
Rho kinase regulates tight junction function and is necessary for tight junction assembly in polarized intestinal epithelia. Gastroenterology 121:566-579.

Background & Aims: Tight junctions are crucial determinants of barrier function in polarized intestinal epithelia and are regulated by Rho guanosine triphosphatase. Rho kinase (ROCK) is a downstream effector of Rho. Methods: A specific inhibitor of ROCK, Y-27632, was used to examine the role of ROCK in the regulation of tight junctions in model intestinal (T84) cells by electrophysiologic, biochemical, morphologic, and molecular biologic approaches. Results: ROCK inhibition induced reorganization of apical F-actin structures and enhanced paracellular permeability but did not alter the distribution or detergent solubility of tight junction proteins. Confocal microscopy showed colocalization of a subpool of ROCK with the tight junction protein zonula occludens 1. Inhibition of ROCK function by a dominant negative mutant of ROCK also produced reorganization of apical F-actin structures without disruption of tight junctions. ROCK inhibition in calcium switch assays showed that ROCK is necessary for the assembly of tight and adherens junctions. Upon calcium repletion, occludin, zonula occludens 1, and E-cadherin failed to redistribute to the intercellular junctions; assembly of the apical F-actin cytoskeleton was prevented; and barrier function failed to recover. Conclusions: It has been suggested that ROCK regulates intact tight junctions via its effects on the F-actin cytoskeleton. ROCK is also critical for assembly of the apical junctional proteins and the F-actin cytoskeleton organization during junctional formation.

20 PMID: 11522741

NOV4

25 Expression of gene NOV4 was assessed using the primer-probe sets Ag217, Ag850, and Ag1469, described in Tables 25, 26, and 27. Results from RTQ-PCR runs are shown in Tables 28, 29, 30, 31, 32, and 33.

Table 25. Probe Name Ag217

30

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-ATCTGTGCTGAGGCATGTTCCCT-3'		22	163	100
Probe	FAM-5'-ATCCTCCTCCCTCCCCGGCTCTC-3'-TAMRA		23	192	101
Reverse	5'-CTGCATGGCTGGTGTGATG-3'		19	222	102

Table 26. Probe Name Ag850

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-CCTTTCTTCTCTTCCTCTCAA-3'	59.1	22	25	103
Probe	FAM-5'-CACCTGGCGAGTGCTCCCTCTG-3'-TAMRA	70	23	71	104
Reverse	5'-GGTGGATGGCGTTGTAGAG-3'	59.1	19	96	105

5 (Please note that there is a single base mismatch within forward primer that is not predicted to affect binding)

Table 27. Probe Name Ag1469

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-CGTACGTCITCCATGATGAGTT-3'	59.1	22	644	106
Probe	TET-5'-CGTGGCCTCGATGATTAAGATCCCTT-3'-TAMRA	69.8	26	666	107
Reverse	5'-AAGTCAGGGATGATGGTGAAG-3'	59	21	699	108

10

Table 28. Panel 1

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	tm303f		tm303f
Endothelial cells	0.0	Renal ca. 786-0	0.0
Endothelial cells (treated)	0.0	Renal ca. A498	0.0
Pancreas	0.0	Renal ca. RXF 393	0.0
Pancreatic ca. CAPAN 2	5.4	Renal ca. ACHN	0.0
Adrenal gland	0.0	Renal ca. UO-31	0.0
Thyroid	0.0	Renal ca. TK-10	0.0
Salavary gland	0.0	Liver	0.0
Pituitary gland	0.0	Liver (fetal)	0.0
Brain (fetal)	0.0	Liver ca. (hepatoblast) HepG2	0.0
Brain (whole)	0.0	Lung	0.0
Brain (amygdala)	0.0	Lung (fetal)	0.0
Brain (cerebellum)	0.0	Lung ca. (small cell) LX-1	3.1
Brain (hippocampus)	0.0	Lung ca. (small cell) NCI-H69	0.2
Brain (substantia nigra)	0.0	Lung ca. (s.cell var.) SHP-77	0.0
Brain (thalamus)	0.0	Lung ca. (large cell)NCI-H460	0.0

Brain (hypothalamus)	0.0	Lung ca. (non-sm. cell) A549	2.2
Spinal cord	0.0	Lung ca. (non-s.cell) NCI-H23	0.0
CNS ca. (glio/astro) U87-MG	0.0	Lung ca (non-s.cell) HOP-62	0.0
CNS ca. (glio/astro) U-118-MG	0.0	Lung ca. (non-s.cl) NCI-H522	0.0
CNS ca. (astro) SW1783	0.3	Lung ca. (squam.) SW 900	0.6
CNS ca.* (neuro; met) SK-N-AS	6.7	Lung ca. (squam.) NCI-H596	0.2
CNS ca. (astro) SF-539	0.0	Mammary gland	0.0
CNS ca. (astro) SNB-75	0.0	Breast ca.* (pl. effusion) MCF-7	0.0
CNS ca. (glio) SNB-19	0.0	Breast ca.* (pl.ef) MDA-MB-231	0.0
CNS ca. (glio) U251	0.6	Breast ca.* (pl. effusion) T47D	0.0
CNS ca. (glio) SF-295	15.3	Breast ca. BT-549	0.0
Heart	0.0	Breast ca. MDA-N	0.0
Skeletal muscle	0.0	Ovary	0.0
Bone marrow	0.0	Ovarian ca. OVCAR-3	0.0
Thymus	0.0	Ovarian ca. OVCAR-4	0.0
Spleen	0.0	Ovarian ca. OVCAR-5	0.1
Lymph node	0.0	Ovarian ca. OVCAR-8	0.0
Colon (ascending)	0.0	Ovarian ca. IGROV-1	0.0
Stomach	0.0	Ovarian ca.* (ascites) SK-OV-3	0.0
Small intestine	0.0	Uterus	7.4
Colon ca. SW480	2.4	Placenta	100.0
Colon ca.* (SW480 met)SW620	4.1	Prostate	0.0
Colon ca. HT29	0.0	Prostate ca.* (bone met)PC-3	0.0
Colon ca. HCT-116	0.0	Testis	4.2
Colon ca. CaCo-2	0.0	Melanoma Hs688(A).T	0.0
Colon ca. HCT-15	0.0	Melanoma* (met) Hs688(B).T	0.0
Colon ca. HCC-2998	0.0	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87	45.4	Melanoma M14	0.0
Bladder	0.0	Melanoma LOX IMVI	0.0
Trachea	0.0	Melanoma* (met) SK-MEL-5	0.0
Kidney	4.1	Melanoma SK-MEL-28	0.0
Kidney (fetal)	0.0		

Table 29. Panel 1.3D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	1.3Dtm2782t_ag1469		1.3Dtm2782t_ag1469
Liver adenocarcinoma	0.0	Kidney (fetal)	1.2
Pancreas	0.0	Renal ca. 786-0	0.0

Pancreatic ca. CAPAN 2	0.0	Renal ca. A498	4.1
Adrenal gland	0.6	Renal ca. RXF 393	2.5
Thyroid	0.6	Renal ca. ACHN	0.0
Salivary gland	0.0	Renal ca. UO-31	0.4
Pituitary gland	0.9	Renal ca. TK-10	0.2
Brain (fetal)	14.5	Liver	0.0
Brain (whole)	9.1	Liver (fetal)	0.1
Brain (amygdala)	8.2	Liver ca. (hepatoblast) HepG2	0.0
Brain (cerebellum)	0.9	Lung	0.0
Brain (hippocampus)	14.9	Lung (fetal)	1.1
Brain (substantia nigra)	0.8	Lung ca. (small cell) LX-1	0.0
Brain (thalamus)	3.6	Lung ca. (small cell) NCI-H69	0.0
Cerebral Cortex	100.0	Lung ca. (s.cell var.) SHP-77	2.1
Spinal cord	0.6	Lung ca. (large cell)NCI-H460	0.0
CNS ca. (glio/astro) U87-MG	0.9	Lung ca. (non-sm. cell) A549	0.0
CNS ca. (glio/astro) U-118-MG	15.1	Lung ca. (non-s.cell) NCI-H23	0.2
CNS ca. (astro) SW1783	0.5	Lung ca (non-s.cell) HOP-62	0.0
CNS ca.* (neuro; met) SK-N-AS	1.3	Lung ca. (non-s.cl) NCI-H522	0.0
CNS ca. (astro) SF-539	0.0	Lung ca. (squam.) SW 900	0.0
CNS ca. (astro) SNB-75	10.2	Lung ca. (squam.) NCI-H596	0.0
CNS ca. (glio) SNB-19	16.3	Mammary gland	8.9
CNS ca. (glio) U251	1.7	Breast ca.* (pl. effusion) MCF-7	12.9
CNS ca. (glio) SF-295	0.3	Breast ca.* (pl.ef) MDA-MB-231	0.6
Heart (fetal)	81.2	Breast ca.* (pl. effusion) T47D	0.0
Heart	2.3	Breast ca. BT-549	1.1
Fetal Skeletal	16.3	Breast ca. MDA-N	0.0
Skeletal muscle	0.1	Ovary	9.8
Bone marrow	0.3	Ovarian ca. OVCAR-3	0.1
Thymus	0.4	Ovarian ca. OVCAR-4	0.0
Spleen	0.6	Ovarian ca. OVCAR-5	0.0
Lymph node	1.9	Ovarian ca. OVCAR-8	0.0
Colorectal	4.4	Ovarian ca. IGROV-1	4.5
Stomach	1.4	Ovarian ca.* (ascites) SK-OV-3	0.6
Small intestine	0.5	Uterus	0.3
Colon ca. SW480	0.0	Placenta	2.4
Colon ca.* (SW480 met)SW620	0.0	Prostate	0.0
Colon ca. HT29	0.0	Prostate ca.* (bone met)PC-3	0.4
Colon ca. HCT-116	0.0	Testis	1.7
Colon ca. CaCo-2	0.0	Melanoma Hs688(A).T	2.5
83219 CC Well to Mod Diff (ODO3866)	6.5	Melanoma* (met) Hs688(B).T	6.8
Colon ca. HCC-2998	0.0	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87	0.0	Melanoma M14	0.0

Bladder	0.4	Melanoma LOX IMVI	0.0
Trachea	0.0	Melanoma* (met) SK-MEL-5	0.4
Kidney	0.1	Adipose	10.6

Table 30. General_screening_panel_v1.4

Tissue Name	Relative Expression(%)	Relative Expression(%)
	1.4tm7173f_ag217_b2	1.4tm7186f_ag850_b2
D6005-01 Human adipose	0.3	0.2
112193 Metastatic melanoma	0.0	0.0
112192 Metastatic melanoma	0.4	0.2
95280 Epidermis (metastatic melanoma)	0.0	0.2
95279 Epidermis (metastatic melanoma)	1.0	0.6
Melanoma (met) SK-MEL-5	0.0	0.0
112196 Tongue (oncology)	0.8	0.4
113461 Testis Pool	1.0	0.5
Prostate ca.(bone met) PC-3	0.0	0.0
113455 Prostate Pool	1.0	0.7
103396 Placenta	33.5	31.8
113463 Uterus Pool	0.1	0.0
Ovarian carcinoma OVCAR-3	0.1	0.1
Ovarian carcinoma(ascites) SK-OV-3	0.1	0.1
95297 Adenocarcinoma (ovary)	0.1	0.0
Ovarian carcinoma OVCAR-5	4.4	4.9
Ovarian carcinoma IGROV-1	0.8	0.2
Ovarian carcinoma OVCAR-8	7.2	3.0
103368 Ovary	0.5	0.6
MCF7 breast carcinoma(pleural effusion)	0.0	0.0
Breast ca. (pleural effusion) MDA-MB-231	0.4	0.0
112189 ductal cell carcinoma(breast)	9.2	11.4
Breast ca. (pleural effusion) T47D	14.5	4.5
Breast carcinoma MDA-N	0.0	0.0
113452 Breast Pool	2.6	1.4
103398 Trachea	0.5	0.4
112354 lung	0.1	0.0
103374 Fetal Lung	0.2	0.4
94921 Small cell carcinoma of the lung	0.7	0.4
Lung ca.(small cell) LX-1	18.4	21.2
94919 Small cell carcinoma of the lung	1.8	0.8
Lung ca.(s.cell var.) SHP-77	1.8	1.0
95268 Lung (Large cell carcinoma)	22.3	24.7
94920 Small cell carcinoma of the lung	0.0	0.1
Lung ca.(non-s.cell) NCI-H23	6.0	3.5

Lung ca.(large cell) NCI-H460	0.6	0.3
Lung ca.(non-s.cell) HOP-62	3.7	1.2
Lung ca.(non-s.cl) NCI-H522	0.0	0.0
103392 Liver	0.0	0.0
103393 Fetal Liver	1.0	1.1
Liver ca.(hepatoblast) HepG2	0.4	0.2
113465 Kidney Pool	1.8	0.8
103373 Fetal Kidney	2.9	2.5
Renal ca. 786-0	0.1	0.0
112188 renal cell carcinoma	0.3	0.2
Renal ca. ACHN	1.2	1.9
112190 Renal cell carcinoma	0.0	0.0
Renal ca. TK-10	0.7	0.2
Bladder	1.0	0.5
Gastric ca.(liver met) NCI-N87	87.0	64.6
112197 Stomach	0.0	0.0
94938 Colon Adenocarcinoma	0.0	0.0
Colon ca. SW480	69.8	58.3
Colon ca.(SW480 met) SW620	29.8	22.4
Colon ca. HT29	1.7	1.0
Colon ca. HCT-116	0.0	0.0
Colon ca. CaCo-2	1.0	0.7
83219 CC Well to Mod Diff (ODO3866)	0.6	0.2
94936 Colon Adenocarcinoma	0.9	0.6
94930 Colon	0.7	0.3
94935 Colon Adenocarcinoma	0.0	0.0
113468 Colon Pool	0.7	0.5
113457 Small Intestine Pool	6.3	2.8
113460 Stomach Pool	1.1	2.1
113467 Bone Marrow Pool	1.3	0.9
103371 Fetal Heart	0.0	0.0
113451 Heart Pool	0.2	0.0
113466 Lymph Node Pool	2.1	3.0
103372 Fetal Skeletal Muscle	0.1	0.0
113456 Skeletal Muscle Pool	0.0	0.1
113459 Spleen Pool	0.0	0.0
113462 Thymus Pool	6.7	3.3
CNS ca. (glio/astro) U87-MG	0.7	0.6
CNS ca. (glio/astro) U-118-MG	0.3	0.2
CNS ca. (neuro;met) SK-N-AS	21.0	16.9
95264 Brain astrocytoma	2.2	2.4
CNS ca. (astro) SNB-75	0.0	0.0
CNS ca. (glio) SNB-19	0.5	0.1
CNS ca. (glio) SF-295	100.0	100.0
113447 Brain (Amygdala) Pool	0.0	0.0

103382 Brain (cerebellum)	0.2	0.2
64019-1 brain(fetal)	0.8	0.7
113448 Brain (Hippocampus) Pool	0.0	0.1
113464 Cerebral Cortex Pool	0.2	0.2
113449 Brain (Substantia nigra) Pool	0.0	0.0
113450 Brain (Thalamus) Pool	0.0	0.0
103384 Brain (whole)	0.3	0.2
113458 Spinal Cord Pool	0.4	0.2
103375 Adrenal Gland	0.4	0.3
113454 Pituitary gland Pool	0.8	0.5
103397 Salivary Gland	0.0	0.0
103369 Thyroid (female)	0.4	0.1
Pancreatic ca. CAPAN2	34.6	25.5
113453 Pancreas Pool	5.7	4.5

Table 31. Panel 2D

Tissue Name	Relative Expression(%)		
	2Dtm2759t_ag1469	2Dtm3205t_ag1469	2Dtm3211t_ag1469
Normal Colon GENPAK 061003	21.2	24.0	25.7
83219 CC Well to Mod Diff (ODO3866)	4.9	6.7	6.3
83220 CC NAT (ODO3866)	2.4	7.6	5.7
83221 CC Gr.2 rectosigmoid (ODO3868)	4.4	6.5	4.5
83222 CC NAT (ODO3868)	13.1	14.5	11.2
83235 CC Mod Diff (ODO3920)	2.2	2.4	2.6
83236 CC NAT (ODO3920)	6.3	6.5	4.9
83237 CC Gr.2 ascend colon (ODO3921)	5.7	9.3	6.4
83238 CC NAT (ODO3921)	8.4	11.3	8.6
83241 CC from Partial Hepatectomy (ODO4309)	5.2	4.5	3.2
83242 Liver NAT (ODO4309)	2.0	3.4	2.7
87472 Colon mets to lung (OD04451-01)	4.5	4.3	4.0
87473 Lung NAT (OD04451-02)	3.0	3.0	3.1
Normal Prostate Clontech A+ 6546-1	0.2	0.3	0.5
84140 Prostate Cancer (OD04410)	2.9	5.4	2.8
84141 Prostate NAT (OD04410)	9.9	13.5	10.2
87073 Prostate Cancer (OD04720-01)	6.0	6.8	4.6
87074 Prostate NAT (OD04720-02)	11.3	8.9	4.2
Normal Lung GENPAK 061010	18.6	19.2	12.7
83239 Lung Met to Muscle (ODO4286)	0.0	1.2	1.0
83240 Muscle NAT (ODO4286)	4.7	6.0	4.4
84136 Lung Malignant Cancer (OD03126)	4.8	8.5	5.8
84137 Lung NAT (OD03126)	8.5	15.9	8.1
84871 Lung Cancer (OD04404)	7.9	7.6	4.9

84872 Lung NAT (OD04404)	16.5	23.0	14.5
84875 Lung Cancer (OD04565)	4.9	3.1	3.4
84876 Lung NAT (OD04565)	3.6	9.5	2.9
85950 Lung Cancer (OD04237-01)	1.4	4.1	2.1
85970 Lung NAT (OD04237-02)	8.4	9.3	7.5
83255 Ocular Mel Met to Liver (ODO4310)	0.6	0.5	0.2
83256 Liver NAT (ODO4310)	1.0	1.0	0.7
84139 Melanoma Mets to Lung (OD04321)	0.2	0.2	0.2
84138 Lung NAT (OD04321)	6.7	9.4	5.4
Normal Kidney GENPAK 061008	11.7	17.3	12.4
83786 Kidney Ca, Nuclear grade 2 (OD04338)	3.0	3.8	4.1
83787 Kidney NAT (OD04338)	13.8	19.5	14.3
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	16.8	19.1	15.0
83789 Kidney NAT (OD04339)	4.9	4.6	4.6
83790 Kidney Ca, Clear cell type (OD04340)	0.9	1.6	0.8
83791 Kidney NAT (OD04340)	11.5	18.3	14.1
83792 Kidney Ca, Nuclear grade 3 (OD04348)	0.6	1.2	0.4
83793 Kidney NAT (OD04348)	8.5	15.4	10.9
87474 Kidney Cancer (OD04622-01)	2.9	4.3	3.4
87475 Kidney NAT (OD04622-03)	1.9	4.5	3.9
85973 Kidney Cancer (OD04450-01)	0.3	0.0	0.4
85974 Kidney NAT (OD04450-03)	5.4	7.8	4.8
Kidney Cancer Clontech 8120607	1.4	2.3	1.7
Kidney NAT Clontech 8120608	3.6	4.2	3.1
Kidney Cancer Clontech 8120613	0.6	0.3	0.7
Kidney NAT Clontech 8120614	59.9	5.4	4.9
Kidney Cancer Clontech 9010320	10.7	9.2	11.7
Kidney NAT Clontech 9010321	8.8	8.1	14.2
Normal Uterus GENPAK 061018	15.0	15.3	14.2
Uterus Cancer GENPAK 064011	9.3	10.2	13.1
Normal Thyroid Clontech A+ 6570-1	3.1	3.6	2.6
Thyroid Cancer GENPAK 064010	20.7	30.1	23.2
Thyroid Cancer INVITROGEN A302152	9.4	20.9	7.3
Thyroid NAT INVITROGEN A302153	1.6	4.0	4.0
Normal Breast GENPAK 061019	45.4	62.4	41.8
84877 Breast Cancer (OD04566)	4.5	5.7	3.0
85975 Breast Cancer (OD04590-01)	10.5	17.8	14.9
85976 Breast Cancer Mets (OD04590-03)	44.4	51.4	35.1
87070 Breast Cancer Metastasis (OD04655-05)	11.0	14.2	12.2
GENPAK Breast Cancer 064006	7.1	8.3	6.0
Breast Cancer Res. Gen. 1024	38.2	37.1	43.8
Breast Cancer Clontech 9100266	5.4	4.8	4.1
Breast NAT Clontech 9100265	4.9	10.3	6.8
Breast Cancer INVITROGEN A209073	11.7	24.7	13.5
Breast NAT INVITROGEN A2090734	20.9	23.3	16.0

Normal Liver GENPAK 061009	8.5	12.6	5.5
Liver Cancer GENPAK 064003	0.4	0.9	0.5
Liver Cancer Research Genetics RNA 1025	3.9	4.2	2.0
Liver Cancer Research Genetics RNA 1026	1.7	4.2	3.7
Paired Liver Cancer Tissue Research Genetics RNA 6004-T	2.8	2.8	2.8
Paired Liver Tissue Research Genetics RNA 6004-N	0.8	1.3	0.8
Paired Liver Cancer Tissue Research Genetics RNA 6005-T	3.7	3.0	1.1
Paired Liver Tissue Research Genetics RNA 6005-N	1.2	2.6	1.6
Normal Bladder GENPAK 061001	5.8	9.7	11.0
Bladder Cancer Research Genetics RNA 1023	2.6	4.3	3.6
Bladder Cancer INVITROGEN A302173	2.3	1.2	1.8
87071 Bladder Cancer (OD04718-01)	0.7	3.6	1.8
87072 Bladder Normal Adjacent (OD04718-03)	12.7	16.6	15.1
Normal Ovary Res. Gen.	13.2	15.9	12.2
Ovarian Cancer GENPAK 064008	100.0	100.0	100.0
87492 Ovary Cancer (OD04768-07)	0.6	0.7	0.6
87493 Ovary NAT (OD04768-08)	18.8	26.4	23.7
Normal Stomach GENPAK 061017	17.2	19.8	20.7
Gastric Cancer Clontech 9060358	4.6	7.0	4.2
NAT Stomach Clontech 9060359	2.7	3.3	3.8
Gastric Cancer Clontech 9060395	17.0	17.3	14.7
NAT Stomach Clontech 9060394	9.9	15.1	9.3
Gastric Cancer Clontech 9060397	8.5	11.1	10.1
NAT Stomach Clontech 9060396	2.1	2.8	2.8
Gastric Cancer GENPAK 064005	8.2	13.0	9.2

Table 32. Panel 4D

Tissue Name	Relative Expression(%)		Relative Expression (%)
	4dx4tm5043f_ag217_b1	4dx4tm5056f_ag217_b1	
93768_Secondary Th1_anti-CD28/anti-CD3	0.0	1.2	0.0
93769_Secondary Th2_anti-CD28/anti-CD3	0.0	0.0	5.5
93770_Secondary Tr1_anti-CD28/anti-CD3	2.6	0.0	1.6
93573_Secondary Th1_resting day 4-6 in IL-2	1.8	0.0	3.3
93572_Secondary Th2_resting day 4-6 in IL-2	0.0	0.0	23.0
93571_Secondary Tr1_resting day 4-6 in IL-2	7.0	1.6	12.6
93568_primary Th1_anti-CD28/anti-CD3	0.0	0.0	4.3
93569_primary Th2_anti-CD28/anti-CD3	0.0	0.0	22.2
93570_primary Tr1_anti-CD28/anti-CD3	0.8	0.0	12.6
93565_primary Th1_resting dy 4-6 in IL-2	0.0	0.0	33.7

93566_primary Th2_resting dy 4-6 in IL-2	0.0	0.0	45.7
93567_primary Tr1_resting dy 4-6 in IL-2	0.0	1.3	74.7
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	8.1	9.2	0.9
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	0.0	0.0	0.0
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.0	0.0	2.4
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0.0	0.0	0.7
93574_chronic CD8 Lymphocytes 2ry activated CD3/CD28	2.1	2.5	0.3
93354_CD4_none	0.0	0.0	3.0
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	5.9
93103_LAK cells_resting	0.0	0.0	6.0
93788_LAK cells_IL-2	0.0	0.0	1.8
93787_LAK cells_IL-2+IL-12	0.0	0.0	11.0
93789_LAK cells_IL-2+IFN gamma	0.0	0.0	11.9
93790_LAK cells_IL-2+ IL-18	2.2	0.0	9.8
93104_LAK cells_PMA/ionomycin and IL-18	0.0	0.0	2.8
93578_NK Cells IL-2_resting	0.0	0.0	13.7
93109_Mixed Lymphocyte Reaction_Two Way MLR	0.0	0.0	6.0
93110_Mixed Lymphocyte Reaction_Two Way MLR	0.0	0.0	1.3
93111_Mixed Lymphocyte Reaction_Two Way MLR	0.0	1.5	0.6
93112_Mononuclear Cells (PBMCs)_resting	0.0	0.0	1.6
93113_Mononuclear Cells (PBMCs)_PWM	0.0	0.0	5.1
93114_Mononuclear Cells (PBMCs)_PHA-L	0.0	0.0	6.2
93249_Ramos (B cell)_none	0.0	0.0	0.0
93250_Ramos (B cell)_ionomycin	0.0	1.5	0.0
93349_B lymphocytes_PWM	0.0	3.4	0.0
93350_B lymphocytes_CD40L and IL-4	0.0	1.7	2.9
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0.0	0.0	0.0
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	0.0	0.0	0.0
93356_Dendritic Cells_none	0.0	0.0	0.7
93355_Dendritic Cells_LPS 100 ng/ml	1.9	1.4	0.0
93775_Dendritic Cells_anti-CD40	0.0	0.0	0.0
93774_Monocytes_resting	0.0	0.0	0.2
93776_Monocytes_LPS 50 ng/ml	0.0	0.0	0.4
93581_Macrophages_resting	0.0	1.5	0.0
93582_Macrophages_LPS 100 ng/ml	6.4	0.0	0.0
93098_HUVEC (Endothelial)_none	0.0	0.0	22.4
93099_HUVEC (Endothelial)_starved	0.0	0.0	45.7
93100_HUVEC (Endothelial)_IL-1b	0.0	0.0	4.1
93779_HUVEC (Endothelial)_IFN gamma	0.0	0.0	38.7
93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.0	0.0	4.9

93101_HUVEC (Endothelial)_TNF alpha + IL4	0.0	0.0	6.4
93781_HUVEC (Endothelial)_IL-11	0.0	2.8	16.6
93583_Lung Microvascular Endothelial Cells_none	0.0	1.1	92.7
93584_Lung Microvascular Endothelial Cells TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.0	25.5
92662_Microvascular Dermal endothelium_none	3.7	0.0	100.0
92663_Microvasvular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.0	20.7
93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	3.9	3.2	0.0
93347_Small Airway Epithelium_none	6.2	4.5	0.2
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	11.2	9.7	1.6
92668_Coronery Artery SMC_resting	5.8	5.9	3.3
92669_Coronery Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	4.2	1.9	2.4
93107_astrocytes_resting	61.1	41.5	27.2
93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	78.6	69.9	10.4
92666_KU-812 (Basophil)_resting	0.0	0.0	0.3
92667_KU-812 (Basophil)_PMA/ionoycin	0.0	0.0	1.7
93579_CCD1106 (Keratinocytes)_none	0.0	0.0	0.0
93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	0.0	0.0	0.0
93791_Liver Cirrhosis	10.9	5.4	4.0
93792_Lupus Kidney	0.0	2.3	10.4
93577_NCI-H292	11.6	2.8	0.0
93358_NCI-H292_IL-4	2.9	3.3	0.0
93360_NCI-H292_IL-9	2.3	1.8	0.0
93359_NCI-H292_IL-13	2.8	0.0	0.0
93357_NCI-H292_IFN gamma	3.8	0.0	0.3
93777_HPAEC_-	0.0	0.0	57.8
93778_HPAEC IL-1 beta/TNA alpha	0.0	0.0	8.8
93254_Normal Human Lung Fibroblast_none	0.0	0.0	7.5
93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	0.0	0.0	6.7
93257_Normal Human Lung Fibroblast_IL-4	0.0	0.0	13.8
93256_Normal Human Lung Fibroblast_IL-9	0.0	0.0	7.2
93255_Normal Human Lung Fibroblast_IL-13	0.0	0.0	20.6
93258_Normal Human Lung Fibroblast_IFN gamma	0.0	1.3	34.6
93106_Dermal Fibroblasts CCD1070_resting	40.7	30.0	1.5
93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	13.1	17.9	8.2
93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	27.0	19.2	0.0
93772_dermal fibroblast_IFN gamma	0.0	0.0	5.6
93771_dermal fibroblast_IL-4	2.3	2.6	7.0
93260_IBD Colitis 2	2.3	0.0	4.0

93261_IBD Crohns	0.0	1.1	0.7
735010_Colon_normal	18.6	5.9	2.3
735019_Lung_none	13.2	8.1	10.6
64028-1_Thymus_none	100.0	100.0	11.8
64030-1_Kidney_none	3.9	1.6	2.8

Table 33. Panel 4.1D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	4.1dx4tm6089f ag850 b2		4.1dx4tm6089f ag850 b2
93768_Secondary Th1_anti-CD28/anti-CD3	0.0	93100_HUVEC (Endothelial) IL-1b	0.0
93769_Secondary Th2_anti-CD28/anti-CD3	0.0	93779_HUVEC (Endothelial) IFN gamma	0.8
93770_Secondary Tr1_anti-CD28/anti-CD3	0.0	93102_HUVEC (Endothelial) TNF alpha + IFN gamma	1.0
93573_Secondary Th1_resting day 4-6 in IL-2	0.0	93101_HUVEC (Endothelial) TNF alpha + IL4	0.0
93572_Secondary Th2_resting day 4-6 in IL-2	0.0	93781_HUVEC (Endothelial) IL-11	0.0
93571_Secondary Tr1_resting day 4-6 in IL-2	0.7	93583_Lung Microvascular Endothelial Cells none	0.0
93568_primary Th1_anti-CD28/anti-CD3	0.2	93584_Lung Microvascular Endothelial Cells_TNF _a (4 ng/ml) and IL1b (1 ng/ml)	0.0
93569_primary Th2_anti-CD28/anti-CD3	0.0	92662_Microvascular Dermal endothelium none	0.3
93570_primary Tr1_anti-CD28/anti-CD3	0.6	92663_Microvasular Dermal endothelium_TNF _a (4 ng/ml) and IL1b (1 ng/ml)	0.0
93565_primary Th1_resting dy 4-6 in IL-2	0.0	93773_Bronchial epithelium_TNF _a (4 ng/ml) and IL1b (1 ng/ml) **	0.9
93566_primary Th2_resting dy 4-6 in IL-2	0.0	93347_Small Airway Epithelium none	1.8
93567_primary Tr1_resting dy 4-6 in IL-2	0.0	93348_Small Airway Epithelium_TNF _a (4 ng/ml) and IL1b (1 ng/ml)	4.0
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	7.4	92668_Coronery Artery SMC resting	1.8
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	0.2	92669_Coronery Artery SMC_TNF _a (4 ng/ml) and IL1b (1 ng/ml)	1.3
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.0	93107_astrocytes resting	31.9
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-	0.2	93108_astrocytes_TNF _a (4 ng/ml) and IL1b (1 ng/ml)	33.4

6 in IL-2			
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.3	92666_KU-812 (Basophil) resting	0.0
93354_CD4 none	0.0	92667_KU-812 (Basophil) PMA/ionoycin	0.0
93252_Secondary Th1/Th2/Tr1 anti-CD95 CH11	0.1	93579_CCD1106 (Keratinocytes) none	0.0
93103_LAK cells resting	0.0	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	0.0
93788_LAK cells IL-2	0.0	93791_Liver Cirrhosis	1.0
93787_LAK cells IL-2+IL-12	0.0	93577_NCI-H292	2.2
93789_LAK cells IL-2+IFN gamma	0.0	93358_NCI-H292 IL-4	1.1
93790_LAK cells IL-2+ IL-18	0.0	93360_NCI-H292 IL-9	1.5
93104_LAK cells_PMA/ionomycin and IL-18	0.6	93359_NCI-H292 IL-13	0.9
93578_NK Cells IL-2 resting	0.0	93357_NCI-H292 IFN gamma	0.3
93109_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93777_HPAEC -	0.0
93110_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93778_HPAEC IL-1 beta/TNA alpha	0.0
93111_Mixed Lymphocyte Reaction_Two Way MLR	0.2	93254_Normal Human Lung Fibroblast none	0.0
93112_Mononuclear Cells (PBMCs) resting	0.0	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	0.0
93113_Mononuclear Cells (PBMCs) PWM	0.0	93257_Normal Human Lung Fibroblast IL-4	0.1
93114_Mononuclear Cells (PBMCs) PHA-L	0.0	93256_Normal Human Lung Fibroblast IL-9	0.0
93249_Ramos (B cell) none	0.0	93255_Normal Human Lung Fibroblast IL-13	0.1
93250_Ramos (B cell) ionomycin	0.0	93258_Normal Human Lung Fibroblast IFN gamma	0.8
93349_B lymphocytes PWM	0.0	93106_Dermal Fibroblasts CCD1070 resting	14.5
93350_B lymphocytes_CD40L and IL-4	0.1	93361_Dermal Fibroblasts CCD1070 TNF alpha 4 ng/ml	15.2
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0.0	93105_Dermal Fibroblasts CCD1070 IL-1 beta 1 ng/ml	10.1
93248_EOL-1 (Eosinophil)_dbcAMP/PMAion mycin	0.0	93772_dermal fibroblast IFN gamma	0.0
93356_Dendritic Cells none	0.0	93771_dermal fibroblast IL-4	0.0
93355_Dendritic Cells_LPS 100 ng/ml	0.3	93892_Dermal fibroblasts none	0.0
93775_Dendritic Cells_anti-CD40	0.0	99202_Neutrophils TNFa+LPS	0.0

93774_Monocytes_resting	0.0	99203_Neutrophils none	0.0
93776_Monocytes_LPS 50 ng/ml	0.0	735010_Colon normal	0.6
93581_Macrophages_resting	0.0	735019_Lung none	0.9
93582_Macrophages_LPS 100 ng/ml	0.8	64028-1_Thymus none	6.0
93098_HUVEC (Endothelial) none	0.0	64030-1_Kidney none	100.0
93099_HUVEC (Endothelial) starved	0.0		

- Panel 1 Summary:** Ag217 Expression of the NOV4 gene is highest in placenta (CT = 21.3). In addition, expression of this gene is also high in testis and uterus tissues. Thus,
- 5 NOV4 gene expression could be used to distinguish placenta, and to a lesser degree testis and uterus tissue from other tissues. In addition, since these tissues are part of the reproductive system, this gene may play a role in reproduction. Therefore, therapeutic modulation of the NOV4 gene or its product might be of use in the treatment of diseases of reproduction, such as infertility. Furthermore, expression of the NOV4 is much higher in adult kidney (CT = 26)
- 10 than fetal kidney (CT = 33) suggesting that this gene may be useful as a marker to distinguish the two.

- Panel 1.3D Summary:** Ag1469 Expression of the NOV4 gene on this panel is highest in cerebral cortex (CT = 27.3). Thus, the expression of this gene might be used to distinguish
- 15 cerebral cortex from other samples. Among CNS samples, this gene is more moderately expressed in fetal brain, amygdala, hippocampus and thalamus. NOV4 gene expression is also detected in hippocampal and cortical tissue on panel CNS_Neurodegeneration_V1.0, but does not show Alzheimer's disease-specific expression. The NOV4 gene encodes a protein with homology to plexin, a transmembrane cell adhesion molecule that interacts with the
- 20 semaphorins in axon guidance and CNS development. Semaphorins can act as axon guidance proteins, specifically as chemorepellents that inhibit CNS regenerative capacity. Decreasing levels of this protein may be of use in inducing a compensatory synaptogenic response, as semaphorins are one of the major obstacles to CNS regeneration. Therefore, reducing the level of the NOV4 transcript or its protein product may be beneficial in the treatment of
- 25 Alzheimer's disease, Parkinson's disease, Huntington's disease, spinocerebellar ataxia, progressive supranuclear palsy, multiple sclerosis, ALS, head trauma, stroke, or any other disease/condition associated with neuronal loss.

The NOV4 gene is also moderately expressed in adipose and ovary. Interestingly, this gene is more highly expressed in fetal heart (CT = 28) when compared to adult heart (CT = 33) as well as in fetal skeletal muscle (CT = 30) when compared to adult skeletal muscle (CT = 37). Thus, the expression of the NOV4 gene might be used to distinguish fetal heart or 5 muscle from adult tissue. Moreover, the therapeutic modulation of this gene, specifically its use in replacement type therapy through the administration of purified protein, might be beneficial in the treatment of diseases involving the degeneration of heart or skeletal muscle, such as the consequence of myocardial infarction or in muscular dystrophy.

10 **General screening panel v1.4 Summary:** Ag217/Ag850 Results from two experiments using different probe/primer sets are in good agreement. Expression of the NOV4 gene on this panel is highest in a sample derived from a brain cancer cell line. In addition, there is substantial expression of this gene in pancreatic, colon, gastric and lung cancer cell lines. Thus, the expression of this gene could be used to distinguish the above 15 mentioned sample types from other tissues. In addition, the therapeutic modulation of the NOV4 gene product, through the use of small molecule drugs or antibodies could be of benefit in the treatment of brain, pancreatic, gastric, colon or lung cancers.

This gene is also expressed at low to moderate levels in a number of other samples on this panel, including kidney, placenta, testis, cerebral cortex and cerebellum.

20 **Panel 2D Summary:** Ag1469 Results from three experiments using the same probe/primer set are in good agreement. Expression of the NOV4 gene is highest in an ovarian cancer sample (CT = 28). Interestingly, expression of this gene is lower in kidney tumors relative to matched normal kidney margins. This pattern of expression is observed in 25 6/9 of the normal adjacent kidney/kidney cancer pairs on this panel. Thus, expression of the NOV4 gene could be used as a marker to distinguish normal kidney tissue from kidney tumors and may also have diagnostic benefit. Finally, therapeutic modulation of this gene product might have benefit in the treatment of kidney cancer.

30 **Panel 2.2 Summary:** Ag217/Ag850 Results from two experiments using different probe/primer sets are in reasonable agreement. Expression of the NOV4 gene is highest in a sample derived from normal kidney tissue adjacent to a kidney cancer, among the samples on this panel. Furthermore, in the majority of cases this gene is expressed more highly in normal kidney tissues adjacent to kidney cancers. These results are consistent with what is seen in 35 Panel 2D. Thus, expression of the NOV4 gene could be used to distinguish normal kidney

tissue from kidney cancer. In addition, therapeutic modulation of the protein encoded by this gene may be of use in the treatment of kidney cancer.

Panel 4D Summary: Ag217/Ag1469 Results from two experiments using different probe/primer sets show some differences. Using the Ag1469 probe/primer set, the NOV4 gene is moderately expressed in the microvascular dermal and lung endothelium (CT 29.2) as well as in primary Tr1 and Th2 T cells. With the Ag217 probe/primer set, the NOV4 gene is expressed at moderate levels in thymus and astrocytes independent of treatment. In addition, lower expression of this gene is seen in dermal fibroblasts. The protein encoded by the NOV4 gene is homologous to murine plexin 2, a transmembrane cell-adhesion molecule. Plexins are receptors for multiple (and perhaps all) classes of semaphorins. Semaphorins influence neural regeneration. Therefore, the expression of this gene in astrocytes suggests that the use of small molecule drugs could be favorable for the treatment of CNS injury. Expression of the NOV4 gene in thymus and some T cells (with Ag1469) suggests a potential role for this plexin in development or differentiation. Therefore, antibodies raised against this protein might be useful as a marker or to modulate T cell differentiation for the treatment of T cell-mediated diseases.

Panel 4.1D Summary: Ag850 The NOV4 gene is expressed in normal kidney, thymus, a dermal fibroblast cell line (CCD1070) and in astrocytes, among the samples on this panel. Expression of this gene is highest in kidney (CT = 28.1), consistent with what is observed in Panel 2.2. The NOV4 gene encodes a protein that has homology to retinoic acid-responsive protein, which is known to be expressed at blood organ barriers and may function in transport (ref. 3). Astrocytes contribute to the blood brain barrier (ref. 4), so based on the homology of this gene to Stra6 and its expression in astrocytes, the NOV4 gene product may be important in maintaining the blood brain barrier and perhaps in the transport of small molecules across this barrier. Therefore, regulation of NOV4 gene product with small molecule therapeutics could allow the passage of specific therapeutic molecules into the brain usually blocked by tight junctions. Furthermore, modulation of the function of this protein may also be important in the treatment of autism, since it has been recently shown that autism may be linked to pathology associated with infection and this particular gene is found within a chromosomal locus associated with autism (ref. 5).

References:

1. Murakami Y., Suto F., Shimizu M., Shinoda T., Kameyama T., Fujisawa H. (2001) Differential expression of plexin-A subfamily members in the mouse nervous system. *Dev. Dyn.* 220:246-258.

5 Plexins comprise a family of transmembrane proteins (the plexin family) which are expressed in nervous tissues. Some plexins have been shown to interact directly with secreted or transmembrane semaphorins, while plexins belonging to the A subfamily are suggested to make complexes with other membrane proteins, neuropilins, and propagate chemorepulsive signals of secreted semaphorins of class 3 into cells or neurons. Despite that much information
10 has been gathered on the plexin-semaphorin interaction, the role of plexins in the nervous system is not well understood. To gain insight into the functions of plexins in the nervous system, spatial and temporal expression patterns of three members of the plexin-A subfamily (plexin-A1, -A2, and -A3) were analyzed in the developing mouse nervous system by *in situ* hybridization analysis in combination with immunohistochemistry. The three plexins are
15 differentially expressed in sensory receptors or neurons in a developmentally regulated manner, suggesting that a particular plexin or set of plexins is shared by neuronal elements and functions as the receptor for semaphorins to regulate neuronal development.

PMID: 11241833

20

2. Ohta K., Mizutani A., Kawakami A., Murakami Y., Kasuya Y., Takagi S., Tanaka H., Fujisawa H. (1995) Plexin: a novel neuronal cell surface molecule that mediates cell adhesion via a homophilic binding mechanism in the presence of calcium ions. *Neuron* 14:1189-1199.

25

Plexin (previously referred to as B2) is a neuronal cell surface molecule that has been identified in *Xenopus*. cDNA cloning reveals that plexin has no homology to known neuronal cell surface molecules but possesses, in its extracellular segment, three internal repeats of cysteine clusters that are homologous to the cysteine-rich domain of the c-met proto-oncogene protein product. The exogenous plexin proteins expressed on the surfaces of L cells by cDNA transfection mediate cell adhesion via a homophilic binding mechanism, under the presence of calcium ions. Plexin is expressed in the receptors and neurons of particular sensory systems. These findings indicate that plexin is a novel calcium-dependent cell adhesion molecule and suggest its involvement in specific neuronal cell interaction and/or contact.

3. Bouillet P., Sapin V, Chazaud C., Messaddeq N., Decimo D., Dolle P., Champon P. (1997) Developmental expression pattern of Stra6, a retinoic acid-responsive gene encoding a new type of membrane protein. *Mech. Dev.* 63: 173-186.

5

Retinoic acid plays important roles in development, growth and differentiation by regulating the expression of target genes. A new retinoic acid-inducible gene, Stra6, has been identified in P19 embryonal carcinoma cells using a subtractive hybridization cDNA cloning technique. Stra6 codes for a very hydrophobic membrane protein of a new type, which does not display similarities with previously characterized integral membrane proteins. Stra6, which exhibits a specific pattern of expression during development and in the adult, is strongly expressed at the level of blood-organ barriers. Interestingly, in testis Sertoli cells, Stra6 has a spermatogenic cycle-dependent expression which is lost in testes of RAR alpha null mutants where Stra6 is expressed in all tubules. The Stra6 protein may be a component of an as yet unidentified transport machinery.

PMID: 9203140

4. Pardridge W.M. (1999) Blood-brain barrier biology and methodology. *J. Neurovirol.* 5: 556-69.

The blood-brain barrier (BBB) is formed by epithelial-like high resistance tight junctions within the endothelium of capillaries perfusing the vertebrate brain. Because of the presence of the BBB, circulating molecules gain access to brain cells only via one of two processes: (i) lipid-mediated transport of small molecules through the BBB by free diffusion, or (ii) catalyzed transport. The latter includes carrier-mediated transport processes for low molecular weight nutrients and water soluble vitamins or receptor-mediated transport for circulating peptides (e.g., insulin), plasma proteins (e.g., transferrin), or viruses. While BBB permeability, per se, is controlled by the biochemical properties of the plasma membranes of the capillary endothelial cells, overall brain microvascular biology is a function of the paracrine interactions between the capillary endothelium and the other two major cells comprising the microcirculation of brain, i.e., the capillary pericyte, which shares the basement membrane with the endothelial cell, and the astrocyte foot process, which invests 99% of the abluminal surface of the capillary basement membrane in brain. Microvascular

functions frequently ascribed to the capillary endothelium are actually executed by either the capillary pericyte or the capillary astrocyte foot process. With respect to BBB methodology, there are a variety of *in vivo* methods for studying biological transport across this important membrane. The classical physiologic techniques may now be correlated with modern
5 biochemical and molecular biological approaches using freshly isolated animal or human brain capillaries. Isolated brain capillary endothelial cells can also be grown in tissue culture to form an '*in vitro* BBB' model. However, BBB research cannot be performed using only the *in vitro* BBB model, but rather it is necessary to correlate observations made with the *in vitro* BBB model with *in vivo* studies.

10

PMID: 10602397

5. Hornig M., Weissenbock H., Horscroft N., Lipkin W.I. (1999) An infection-based model of neurodevelopmental damage. Proc. Natl. Acad. Sci. U S A 96: 12102-12107.

15

Perinatal exposure to infectious agents and toxins is linked to the pathogenesis of neuropsychiatric disorders, but the mechanisms by which environmental triggers interact with developing immune and neural elements to create neurodevelopmental disturbances are poorly understood. Hornig et al. describe a model for investigating disorders of central nervous
20 system development based on neonatal rat infection with Borna disease virus, a neurotropic noncytolytic RNA virus. Infection results in abnormal righting reflexes, hyperactivity, inhibition of open-field exploration, and stereotypic behaviors. Architecture is markedly disrupted in hippocampus and cerebellum, with reduction in granule and Purkinje cell numbers. Neurons are lost predominantly by apoptosis, as supported by increased mRNA
25 levels for pro-apoptotic products (Fas, caspase-1), decreased mRNA levels for the anti-apoptotic bcl-x, and *in situ* labeling of fragmented DNA. Although inflammatory infiltrates are observed transiently in frontal cortex, glial activation (microgliosis > astrogliosis) is prominent throughout the brain and persists for several weeks in concert with increased levels of proinflammatory cytokine mRNAs (interleukins 1alpha, 1beta, and 6 and tumor necrosis
30 factor alpha) and progressive hippocampal and cerebellar damage. The resemblance of these functional and neuropathologic abnormalities to human neurodevelopmental disorders suggests the utility of this model for defining cellular, biochemical, histologic, and functional outcomes of interactions of environmental influences with the developing central nervous system.

PMID: 10518583

5

NOV5

Expression of gene NOV5 was assessed using the primer-probe set Ag2976, described in Table 34. Results from RTQ-PCR runs are shown in Tables 35, 36, 37, 38, and 39.

10

Table 34. Probe Name Ag2976

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-ACCCCAAATGGATTCCATTA-3'	59	20	1428	109
Probe	FAM-5'-CCCTCATGGATCTGCATAACCACACA-3'-TAMRA	69.9	26	1465	110
Reverse	5'-CTTGTTGTGCGATGCTTGTC-3'	58.9	20	1516	111

Table 35. Panel 1.3D

Tissue Name	Relative Expression(%)	
	1.3dtm3946f_a g2976	1.3dx4tm5499f ag2976_b2
Liver adenocarcinoma	0.0	0.0
Pancreas	0.0	0.0
Pancreatic ca. CAPAN 2	0.0	0.0
Adrenal gland	0.0	0.7
Thyroid	0.0	0.0
Salivary gland	0.0	0.0
Pituitary gland	0.4	0.0
Brain (fetal)	0.7	1.0
Brain (whole)	1.1	6.5
Brain (amygdala)	6.9	4.4
Brain (cerebellum)	0.0	0.9
Brain (hippocampus)	18.9	3.3
Brain (substantia nigra)	1.9	7.5
Brain (thalamus)	2.0	5.5
Cerebral Cortex	5.0	5.3
Spinal cord	0.2	0.3
CNS ca. (glial/astro) U87-MG	1.5	0.7
CNS ca. (glial/astro) U-118-MG	0.6	0.4
CNS ca. (astro) SW1783	0.3	0.0

CNS ca.* (neuro; met) SK-N-AS	0.0	0.0
CNS ca. (astro) SF-539	0.0	0.0
CNS ca. (astro) SNB-75	0.0	0.0
CNS ca. (glio) SNB-19	0.0	0.0
CNS ca. (glio) U251	0.0	0.5
CNS ca. (glio) SF-295	0.0	0.0
Heart (fetal)	0.2	0.0
Heart	0.0	0.0
Fetal Skeletal	6.8	3.5
Skeletal muscle	0.1	0.8
Bone marrow	0.0	0.0
Thymus	0.0	0.5
Spleen	0.0	1.8
Lymph node	100.0	0.2
Colorectal	0.8	1.3
Stomach	54.0	100.0
Small intestine	0.4	0.5
Colon ca. SW480	0.0	0.0
Colon ca.* (SW480 met)SW620	1.0	1.8
Colon ca. HT29	0.2	0.0
Colon ca. HCT-116	0.0	0.0
Colon ca. CaCo-2	0.0	0.0
83219 CC Well to Mod Diff (ODO3866)	0.6	0.0
Colon ca. HCC-2998	0.2	0.0
Gastric ca.* (liver met) NCI-N87	0.4	0.3
Bladder	0.4	0.4
Trachea	0.0	0.0
Kidney	0.0	0.0
Kidney (fetal)	0.0	0.0
Renal ca. 786-0	0.3	0.0
Renal ca. A498	0.2	0.5
Renal ca. RXF 393	0.0	0.0
Renal ca. ACHN	0.0	0.0
Renal ca. UO-31	0.0	0.0
Renal ca. TK-10	0.0	0.0
Liver	0.2	0.0
Liver (fetal)	0.0	0.0
Liver ca. (hepatoblast) HepG2	0.0	0.0
Lung	0.3	0.2
Lung (fetal)	0.6	0.0
Lung ca. (small cell) LX-1	0.9	3.6
Lung ca. (small cell) NCI-H69	3.6	2.4
Lung ca. (s.cell var.) SHP-77	2.9	1.4
Lung ca. (large cell)NCI-H460	0.0	19.9
Lung ca. (non-sm. cell) A549	0.0	0.0

Lung ca. (non-s.cell) NCI-H23	0.6	0.2
Lung ca (non-s.cell) HOP-62	0.0	0.7
Lung ca. (non-s.cl) NCI-H522	0.0	0.0
Lung ca. (squam.) SW 900	0.0	0.0
Lung ca. (squam.) NCI-H596	0.2	0.2
Mammary gland	0.2	0.0
Breast ca.* (pl. effusion) MCF-7	0.3	0.4
Breast ca.* (pl.ef) MDA-MB-231	0.1	0.0
Breast ca.* (pl. effusion) T47D	0.0	0.0
Breast ca. BT-549	0.2	0.2
Breast ca. MDA-N	0.3	0.0
Ovary	0.1	0.0
Ovarian ca. OVCAR-3	0.6	0.0
Ovarian ca. OVCAR-4	0.0	0.0
Ovarian ca. OVCAR-5	0.0	0.0
Ovarian ca. OVCAR-8	2.0	0.0
Ovarian ca. IGROV-1	0.0	0.0
Ovarian ca.* (ascites) SK-OV-3	0.0	0.0
Uterus	0.0	0.0
Placenta	0.3	0.0
Prostate	0.0	0.0
Prostate ca.* (bone met)PC-3	0.1	0.0
Testis	8.8	13.6
Melanoma Hs688(A).T	0.0	0.0
Melanoma* (met) Hs688(B).T	0.0	0.0
Melanoma UACC-62	0.1	0.0
Melanoma M14	0.2	0.0
Melanoma LOX IMVI	0.0	0.0
Melanoma* (met) SK-MEL-5	0.2	0.5
Adipose	0.3	0.3

Table 36. Panel 2D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	2dtm3947f_ag2976		2dtm3947f_ag2976
Normal Colon GENPAK 061003	12.9	Kidney NAT Clontech 8120608	0.0
83219 CC Well to Mod Diff (ODO3866)	20.2	Kidney Cancer Clontech 8120613	0.0
83220 CC NAT (ODO3866)	12.9	Kidney NAT Clontech 8120614	0.0
83221 CC Gr.2 rectosigmoid (ODO3868)	0.0	Kidney Cancer Clontech 9010320	0.0
83222 CC NAT (ODO3868)	0.0	Kidney NAT Clontech 9010321	0.3

83235 CC Mod Diff (ODO3920)	0.0	Normal Uterus GENPAK 061018	0.0
83236 CC NAT (ODO3920)	0.0	Uterus Cancer GENPAK 064011	5.2
83237 CC Gr.2 ascend colon (ODO3921)	10.6	Normal Thyroid Clontech A+ 6570-1	0.0
83238 CC NAT (ODO3921)	17.0	Thyroid Cancer GENPAK 064010	0.0
83241 CC from Partial Hepatectomy (ODO4309)	0.0	Thyroid Cancer INVITROGEN A302152	0.0
83242 Liver NAT (ODO4309)	0.7	Thyroid NAT INVITROGEN A302153	0.0
87472 Colon mets to lung (OD04451-01)	0.3	Normal Breast GENPAK 061019	0.0
87473 Lung NAT (OD04451- 02)	0.0	84877 Breast Cancer (OD04566)	0.0
Normal Prostate Clontech A+ 6546-1	0.0	85975 Breast Cancer (OD04590-01)	0.0
84140 Prostate Cancer (OD04410)	0.5	85976 Breast Cancer Mets (OD04590-03)	1.1
84141 Prostate NAT (OD04410)	1.6	87070 Breast Cancer Metastasis (OD04655-05)	0.0
87073 Prostate Cancer (OD04720-01)	0.8	GENPAK Breast Cancer 064006	0.0
87074 Prostate NAT (OD04720-02)	1.4	Breast Cancer Res. Gen. 1024	6.2
Normal Lung GENPAK 061010	5.2	Breast Cancer Clontech 9100266	0.9
83239 Lung Met to Muscle (ODO4286)	9.8	Breast NAT Clontech 9100265	0.0
83240 Muscle NAT (ODO4286)	0.0	Breast Cancer INVITROGEN A209073	1.4
84136 Lung Malignant Cancer (OD03126)	0.0	Breast NAT INVITROGEN A2090734	0.2
84137 Lung NAT (OD03126)	0.0	Normal Liver GENPAK 061009	0.0
84871 Lung Cancer (OD04404)	0.3	Liver Cancer GENPAK 064003	5.7
84872 Lung NAT (OD04404)	0.5	Liver Cancer Research Genetics RNA 1025	0.0
84875 Lung Cancer (OD04565)	0.8	Liver Cancer Research Genetics RNA 1026	0.0
84876 Lung NAT (OD04565)	0.0	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	1.3
85950 Lung Cancer (OD04237- 01)	1.7	Paired Liver Tissue Research Genetics RNA 6004-N	2.5
85970 Lung NAT (OD04237- 02)	0.7	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	0.0
83255 Ocular Mel Met to Liver (ODO4310)	0.0	Paired Liver Tissue Research Genetics RNA 6005-N	3.1
83256 Liver NAT (ODO4310)	0.0	Normal Bladder GENPAK 061001	4.8

84139 Melanoma Mets to Lung (OD04321)	0.0	Bladder Cancer Research Genetics RNA 1023	2.1
84138 Lung NAT (OD04321)	0.0	Bladder Cancer INVITROGEN A302173	15.2
Normal Kidney GENPAK 061008	0.8	87071 Bladder Cancer (OD04718-01)	2.0
83786 Kidney Ca, Nuclear grade 2 (OD04338)	0.7	87072 Bladder Normal Adjacent (OD04718-03)	0.0
83787 Kidney NAT (OD04338)	0.3	Normal Ovary Res. Gen.	4.6
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	0.3	Ovarian Cancer GENPAK 064008	0.4
83789 Kidney NAT (OD04339)	2.0	87492 Ovary Cancer (OD04768-07)	0.9
83790 Kidney Ca, Clear cell type (OD04340)	0.2	87493 Ovary NAT (OD04768-08)	0.0
83791 Kidney NAT (OD04340)	1.5	Normal Stomach GENPAK 061017	100.0
83792 Kidney Ca, Nuclear grade 3 (OD04348)	0.0	Gastric Cancer Clontech 9060358	0.0
83793 Kidney NAT (OD04348)	0.9	NAT Stomach Clontech 9060359	70.2
87474 Kidney Cancer (OD04622-01)	0.0	Gastric Cancer Clontech 9060395	0.0
87475 Kidney NAT (OD04622-03)	0.0	NAT Stomach Clontech 9060394	26.4
85973 Kidney Cancer (OD04450-01)	0.3	Gastric Cancer Clontech 9060397	0.0
85974 Kidney NAT (OD04450-03)	0.1	NAT Stomach Clontech 9060396	33.0
Kidney Cancer Clontech 8120607	0.0	Gastric Cancer GENPAK 064005	2.5

Table 37. Panel 3D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	3dx4tm5126f_ag2976_a1		3dx4tm5126f_ag2976_a1
94905_Daoy_Medulloblastoma/Cerebellum sscDNA	7.9	94954_Ca Ski_Cervical epidermoid carcinoma (metastasis) sscDNA	0.0
94906_TE671_Medulloblastoma/Cerebellum sscDNA	0.0	94955_ES-2_Ovarian clear cell carcinoma sscDNA	0.0
94907_D283_Med_Medulloblastoma/Cerebellum sscDNA	0.0	94957_Ramos/6h stim_ Stimulated with PMA/ionomycin 6h sscDNA	0.0
94908_PFSK-1_Primitive Neuroectodermal/Cerebellum_s scDNA	0.0	94958_Ramos/14h stim_ Stimulated with PMA/ionomycin 14h sscDNA	5.1
94909_XF-498_CNS sscDNA	0.0	94962_MEG-01_Chronic myelogenous leukemia	0.0

		(megakaryoblast)_sscDNA	
94910_SNBT-78_CNS/glioma_sscDNA	0.0	94963_Raji_Burkitt's lymphoma_sscDNA	0.0
94911_SF-268_CNS/glioblastoma_sscDNA	0.0	94964_Daudi_Burkitt's lymphoma_sscDNA	0.0
94912_T98G_Glioblastoma_sscDNA	0.0	94965_U266_B-cell plasmacytoma/myeloma_sscDNA	0.0
96776_SK-N-SH_Neuroblastoma (metastasis)_sscDNA	0.0	94968_CA46_Burkitt's lymphoma_sscDNA	6.0
94913_SF-295_CNS/glioblastoma_sscDNA	0.0	94970_RL_non-Hodgkin's B-cell lymphoma_sscDNA	0.0
94914_Cerebellum_sscDNA	19.4	94972_JM1_pre-B-cell lymphoma/leukemia_sscDNA	0.0
96777_Cerebellum_sscDNA	0.0	94973_Jurkat_T cell leukemia_sscDNA	0.0
94916_NCI-H292_Mucoepidermoid lung carcinoma_sscDNA	0.0	94974_TF-1_Erythroleukemia_sscDNA	0.0
94917_DMS-114_Small cell lung cancer_sscDNA	15.0	94975_HUT 78_T-cell lymphoma_sscDNA	2.8
94918_DMS-79_Small cell lung cancer/neuroendocrine_sscDNA	69.5	94977_U937_Histiocytic lymphoma_sscDNA	0.0
94919_NCI-H146_Small cell lung cancer/neuroendocrine_sscDNA	0.0	94980_KU-812_Myelogenous leukemia_sscDNA	0.0
94920_NCI-H526_Small cell lung cancer/neuroendocrine_sscDNA	75.8	94981_769-P_Clear cell renal carcinoma_sscDNA	0.0
94921_NCI-N417_Small cell lung cancer/neuroendocrine_sscDNA	0.0	94983_Caki-2_Clear cell renal carcinoma_sscDNA	0.0
94923_NCI-H82_Small cell lung cancer/neuroendocrine_sscDNA	0.0	94984_SW 839_Clear cell renal carcinoma_sscDNA	0.0
94924_NCI-H157_Squamous cell lung cancer (metastasis)_sscDNA	19.4	94986_G401_Wilms' tumor_sscDNA	0.0
94925_NCI-H1155_Large cell lung cancer/neuroendocrine_sscDNA	100.0	94987_Hs766T_Pancreatic carcinoma (LN metastasis)_sscDNA	4.5
94926_NCI-H1299_Large cell lung cancer/neuroendocrine_sscDNA	5.8	94988_CAPAN-1_Pancreatic adenocarcinoma (liver metastasis)_sscDNA	0.0
94927_NCI-H727_Lung carcinoid_sscDNA	17.1	94989_SU86.86_Pancreatic carcinoma (liver metastasis)_sscDNA	4.5
94928_NCI-UMC-11_Lung carcinoid_sscDNA	0.0	94990_BxPC-3_Pancreatic adenocarcinoma_sscDNA	0.0
94929_LX-1_Small cell lung	0.0	94991_HPAC_Pancreatic	0.0

cancer_sscDNA		adenocarcinoma_sscDNA	
94930_Colo-205_Colon cancer sscDNA	0.0	94992_MIA PaCa-2_Pancreatic carcinoma sscDNA	0.0
94931_KM12_Colon cancer sscDNA	0.0	94993_CFPAC-1_Pancreatic ductal adenocarcinoma sscDNA	0.0
94932_KM20L2_Colon cancer sscDNA	0.0	94994_PANC-1_Pancreatic epithelioid ductal carcinoma sscDNA	5.0
94933_NCI-H716_Colon cancer sscDNA	0.0	94996_T24_Bladder carcinoma (transitional cell) sscDNA	0.0
94935_SW-48_Colon adenocarcinoma sscDNA	0.0	94997_5637_Bladder carcinoma sscDNA	0.0
94936_SW1116_Colon adenocarcinoma sscDNA	0.0	94998_HT-1197_Bladder carcinoma sscDNA	32.2
94937_LS 174T_Colon adenocarcinoma sscDNA	0.0	94999_UM-UC-3_Bladder carcinoma (transitional cell) sscDNA	0.0
94938_SW-948_Colon adenocarcinoma sscDNA	0.0	95000_A204_Rhabdomyosarcoma sscDNA	0.0
94939_SW-480_Colon adenocarcinoma sscDNA	19.4	95001_HT-1080_Fibrosarcoma sscDNA	0.0
94940_NCI-SNU-5_Gastric carcinoma sscDNA	0.0	95002_MG-63_Osteosarcoma (bone) sscDNA	0.0
94941_KATO III_Gastric carcinoma sscDNA	0.0	95003_SK-LMS-1 Leiomyosarcoma (vulva) sscDNA	0.0
94943_NCI-SNU-16_Gastric carcinoma sscDNA	5.2	95004_SJRH30_Rhabdomyosarcoma (met to bone marrow) sscDNA	0.0
94944_NCI-SNU-1_Gastric carcinoma sscDNA	0.0	95005_A431_Epidermoid carcinoma sscDNA	13.9
94946_RF-1_Gastric adenocarcinoma sscDNA	0.0	95007_WM266-4 Melanoma sscDNA	0.0
94947_RF-48_Gastric adenocarcinoma sscDNA	5.1	95010_DU 145_Prostate carcinoma (brain metastasis) sscDNA	0.0
96778_MKN-45_Gastric carcinoma sscDNA	0.0	95012_MDA-MB-468_Breast adenocarcinoma sscDNA	0.0
94949_NCI-N87_Gastric carcinoma sscDNA	0.0	95013_SCC-4_Squamous cell carcinoma of tongue sscDNA	0.0
94951_OVCAR-5_Ovarian carcinoma sscDNA	11.4	95014_SCC-9_Squamous cell carcinoma of tongue sscDNA	0.0
94952_RL95-2_Uterine carcinoma sscDNA	0.0	95015_SCC-15_Squamous cell carcinoma of tongue sscDNA	0.0
94953_HelaS3_Cervical adenocarcinoma sscDNA	0.0	95017_CAL 27_Squamous cell carcinoma of tongue sscDNA	0.0

Table 38. Panel 4D

Tissue Name	Relative Expression (%)	Tissue Name	Relative Expression (%)
	4dtm3948f_ag2976		4dtm3948f_ag2976
93768_Secondary Th1_anti-CD28/anti-CD3	1.5	93100_HUVEC (Endothelial)_IL-1b	0.0
93769_Secondary Th2_anti-CD28/anti-CD3	0.0	93779_HUVEC (Endothelial)_IFN gamma	0.0
93770_Secondary Tr1_anti-CD28/anti-CD3	0.0	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.0
93573_Secondary Th1_resting day 4-6 in IL-2	1.3	93101_HUVEC (Endothelial)_TNF alpha + IL4	0.0
93572_Secondary Th2_resting day 4-6 in IL-2	1.5	93781_HUVEC (Endothelial)_IL-11	0.0
93571_Secondary Tr1_resting day 4-6 in IL-2	0.0	93583_Lung Microvascular Endothelial Cells none	0.0
93568_primary Th1_anti-CD28/anti-CD3	0.0	93584_Lung Microvascular Endothelial Cells TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93569_primary Th2_anti-CD28/anti-CD3	0.0	92662_Microvascular Dermal endothelium none	0.0
93570_primary Tr1_anti-CD28/anti-CD3	0.0	92663_Microvasular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93565_primary Th1_resting dy 4-6 in IL-2	0.0	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	0.0
93566_primary Th2_resting dy 4-6 in IL-2	0.0	93347_Small Airway Epithelium none	0.0
93567_primary Tr1_resting dy 4-6 in IL-2	0.0	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	0.0	92668_Coronery Artery SMC resting	3.0
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	0.0	92669_Coronery Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.0	93107 astrocytes resting	1.5
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0.0	93108 astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.0	92666_KU-812 (Basophil) resting	2.6
93354_CD4_none	3.0	92667_KU-812 (Basophil) PMA/ionoycin	0.0
93252_Secondary Th1/Th2/Tr1 anti-CD95 CH11	0.0	93579_CCD1106 (Keratinocytes) none	0.0

93103_LAK cells_resting	0.0	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	3.3
93788_LAK cells IL-2	0.0	93791_Liver Cirrhosis	40.6
93787_LAK cells IL-2+IL-12	0.0	93792_Lupus Kidney	1.0
93789_LAK cells IL-2+IFN gamma	0.0	93577_NCI-H292	0.2
93790_LAK cells IL-2+ IL-18	0.0	93358_NCI-H292 IL-4	0.0
93104_LAK cells_PMA/ionomycin and IL- 18	2.8	93360_NCI-H292 IL-9	2.6
93578_NK Cells IL-2 resting	0.0	93359_NCI-H292 IL-13	0.0
93109_Mixed Lymphocyte Reaction Two Way MLR	0.0	93357_NCI-H292 IFN gamma	0.2
93110_Mixed Lymphocyte Reaction Two Way MLR	0.0	93777_HPAEC -	1.7
93111_Mixed Lymphocyte Reaction Two Way MLR	0.0	93778_HPAEC IL-1 beta/TNA alpha	0.0
93112_Mononuclear Cells (PBMCs) resting	0.0	93254_Normal Human Lung Fibroblast none	1.3
93113_Mononuclear Cells (PBMCs) PWM	1.6	93253_Normal Human Lung Fibroblast TNFa (4 ng/ml) and IL-1b (1 ng/ml)	0.0
93114_Mononuclear Cells (PBMCs) PHA-L	0.0	93257_Normal Human Lung Fibroblast IL-4	1.7
93249_Ramos (B cell) none	6.2	93256_Normal Human Lung Fibroblast IL-9	0.0
93250_Ramos (B cell) ionomycin	10.7	93255_Normal Human Lung Fibroblast IL-13	2.8
93349_B lymphocytes PWM	0.0	93258_Normal Human Lung Fibroblast IFN gamma	0.0
93350_B lymphocytes_CD40L and IL-4	0.0	93106_Dermal Fibroblasts CCD1070 resting	0.0
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0.0	93361_Dermal Fibroblasts CCD1070 TNF alpha 4 ng/ml	0.0
93248_EOL-1 (Eosinophil)_dbcAMP/PMAion omyclin	0.0	93105_Dermal Fibroblasts CCD1070 IL-1 beta 1 ng/ml	0.0
93356_Dendritic Cells none	0.0	93772_dermal fibroblast IFN gamma	1.4
93355_Dendritic Cells_LPS 100 ng/ml	5.0	93771_dermal fibroblast IL-4	12.5
93775_Dendritic Cells_anti- CD40	1.1	93260_IBD Colitis 2	4.9
93774_Monocytes resting	0.6	93261_IBD Crohns	1.6
93776_Monocytes_LPS 50 ng/ml	2.6	735010_Colon_normal	100.0
93581_Macrophages resting	0.4	735019_Lung_none	40.6
93582_Macrophages_LPS 100 ng/ml	0.0	64028-1_Thymus_none	2.1
93098_HUVEC	1.5	64030-1_Kidney_none	1.6

(Endothelial)_none			
93099_HUVEC			
(Endothelial) starved	0.0		

Table 39. Panel CNSD.01

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	cns1x4tm6194f ag2976_a2		cns1x4tm6194f ag2976_a2
102633 BA4 Control	12.0	102605 BA17 PSP	0.0
102641 BA4 Control2	51.2	102612 BA17 PSP2	5.3
102625 BA4 Alzheimer's2	2.6	102637 Sub Nigra Control	13.9
102649 BA4 Parkinson's	23.8	102645 Sub Nigra Control2	50.3
102656 BA4 Parkinson's2	51.6	102629 Sub Nigra Alzheimer's2	13.9
102664 BA4 Huntington's	25.2	102660 Sub Nigra Parkinson's2	72.5
102671 BA4 Huntington's2	0.0	102667 Sub Nigra Huntington's	87.2
102603 BA4 PSP	0.0	102674 Sub Nigra Huntington's2	47.6
102610 BA4 PSP2	10.2	102614 Sub Nigra PSP2	6.1
102588 BA4 Depression	6.3	102592 Sub Nigra Depression	1.0
102596 BA4 Depression2	0.0	102599 Sub Nigra Depression2	0.0
102634 BA7 Control	14.2	102636 Glob Palladus Control	6.3
102642 BA7 Control2	55.8	102644 Glob Palladus Control2	24.9
102626 BA7 Alzheimer's2	9.4	102620 Glob Palladus Alzheimer's	15.8
102650 BA7 Parkinson's	3.6	102628 Glob Palladus Alzheimer's2	1.0
102657 BA7 Parkinson's2	28.3	102652 Glob Palladus Parkinson's	17.6
102665 BA7 Huntington's	34.7	102659 Glob Palladus Parkinson's2	4.8
102672 BA7 Huntington's2	13.6	102606 Glob Palladus PSP	0.0
102604 BA7 PSP	6.6	102613 Glob Palladus PSP2	0.0
102611 BA7 PSP2	0.0	102591 Glob Palladus Depression	5.0
102589 BA7 Depression	0.0	102638 Temp Pole Control	9.7
102632 BA9 Control	16.1	102646 Temp Pole Control2	55.7
102640 BA9 Control2	100.0	102622 Temp Pole Alzheimer's	6.3
102617 BA9 Alzheimer's	1.9	102630 Temp Pole Alzheimer's2	0.0
102624 BA9 Alzheimer's2	11.9	102653 Temp Pole Parkinson's	2.9
102648 BA9 Parkinson's	9.3	102661 Temp Pole Parkinson's2	17.3
102655 BA9 Parkinson's2	29.7	102668 Temp Pole Huntington's	58.1

102663 BA9 Huntington's	41.4	102607 Temp Pole PSP	9.8
102670 BA9 Huntington's2	0.0	102615 Temp Pole PSP2	0.0
		102600 Temp Pole Depression2	12.4
102602 BA9 PSP	5.3		
102609 BA9 PSP2	0.0	102639 Cing Gyr Control	37.1
102587 BA9 Depression	5.9	102647 Cing Gyr Control2	20.2
102595 BA9 Depression2	0.0	102623 Cing Gyr Alzheimer's	7.2
102635 BA17 Control	13.4	102631 Cing Gyr Alzheimer's2	12.4
102643 BA17 Control2	30.9	102654 Cing Gyr Parkinson's	5.4
102627 BA17 Alzheimer's2	6.2	102662 Cing Gyr Parkinson's2	32.8
102651 BA17 Parkinson's	24.8	102669 Cing Gyr Huntington's	49.7
		102676 Cing Gyr Huntington's2	
102658 BA17 Parkinson's2	26.0		14.1
102666 BA17 Huntington's	51.1	102608 Cing Gyr PSP	9.0
102673 BA17 Huntington's2	11.8	102616 Cing Gyr PSP2	5.3
102590 BA17 Depression	0.0	102594 Cing Gyr Depression	0.0
102597 BA17 Depression2	4.8	102601 Cing Gyr Depression2	0.0

Panel 1.3D Summary: Ag2976 Results from two experiments using the same probe/primer set show some discrepancies; therefore, only those results that are common between the two experiments will be considered here. The NOV5 gene is expressed at moderate levels in stomach (CT = 28-29) and testis (CT = 30-31). In addition, low but significant expression of this gene is seen in several parts of the CNS, including amygdala, hippocampus, substantia nigra, thalamus, and cerebral cortex. The NOV5 gene encodes a protein with homology to the dopamine receptor of the D1/D5 class. The dopamine (D2) receptor is the most well-established site of action of all known antipsychotics, suggesting a central role for the dopaminergic system in neuropsychiatric disease. The homology of this receptor with the dopamine D5 receptor makes it an excellent candidate drug target for psychiatric diseases, especially depression, bipolar disorder, schizophrenia, and schizoaffective disorder. In addition, NOV5 gene expression appears to be down regulated in a number of brain cancer cell lines.

Panel 2D Summary: Ag2976 Expression of the NOV5 gene is highest in stomach (CT = 30), among the samples on this panel; this result is consistent with what is observed in Panel 1.3D. Interestingly, expression of this gene is lower in 3/3 gastric tumors when compared to the normal margins. Thus, expression of the NOV5 gene could be used to distinguish normal stomach tissue from gastric cancer tissue. In addition, therapeutic modulation of the NOV5 gene product might be of benefit for the treatment of gastric cancers.

Panel 3D Summary: Ag2976 Low but significant expression of the NOV5 gene is limited to three lung cancer cell lines. Thus, expression of this gene might be of use in the distinction of lung cancer cell lines from other cell lines.

5

Panel 4D Summary: Ag2976 Expression of the NOV5 gene is highest in colon (CT = 30.2). Expression of this gene is decreased expression in IBD colitis and IBD Crohn's, suggesting a potential role in these diseases. In addition, the NOV5 gene is expressed at low levels in lung, dermal fibroblasts treated with IL-4, liver cirrhosis and Ramos B cells.

10

Panel CNSD.01 Summary: Ag2976 The NOV5 gene is expressed at low to moderate levels in the brain, and is present in at least hippocampus, cerebral cortex, substantia nigra, thalamus, globus pallidus and amygdala. In Panel CNS_1, this gene shows decreased expression in several regions of the brain of depressed patients. The dopamine (D2) receptor is the most well-established site of action of all known antipsychotics, suggesting a central role for the dopaminergic system in neuropsychiatric disease. The homology of this receptor with the dopamine D5 receptor, in addition to its downregulation in depression, makes it an excellent candidate drug target for psychiatric diseases, especially depression, bipolar disorder, schizophrenia, and schizoaffective disorder.

15

NOV7a and NOV7b

Expression of gene NOV7a and NOV7b was assessed using the primer-probe sets Ag760 and Ag1537, described in Tables 40 and 41. Results from RTQ-PCR runs are shown in Tables 42, 43, 44, and 45.

Table 40. Probe Name Ag760

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-CACCATGACAACGACACCTATA-3'	58.4	22	1924	112
Probe	TET-5'-ATATGGCACCAACATCACATGCACG-3'-TAMRA	69.7	25	1947	113
Reverse	5'-TGGGTAGAAAGTGTGTGAAA-3'	58.2	22	1979	114

20

Table 41. Probe Name Ag1537

Primers	Sequences	TM	Length	Start Position	SEQ ID. NO:
Forward	5'-AAGGAGCTGGAAGAGAAGAAGA-3'	58.9	22	38	115
Probe	FAM-5'-ATCAGAAACTCAGCCCTGGACACCTG-3'-TAMRA	69.6	26	92	116
Reverse	5'-GCTGCGACTTGGTCTTGAT-3'	59	19	119	117

5

Table 42. Panel 1.2

Tissue Name	Relative Expression(%)	Relative Expression(%)
	1.2tm880t_ag760	1.2tm2211f_ag1537
Endothelial cells	1.3	2.5
Heart (fetal)	2.3	17.6
Pancreas	74.2	35.4
Pancreatic ca. CAPAN 2	0.0	0.0
Adrenal Gland (new lot*)	19.1	37.4
Thyroid	100.0	14.9
Salavary gland	15.8	34.6
Pituitary gland	27.4	2.1
Brain (fetal)	0.7	0.0
Brain (whole)	0.5	0.2
Brain (amygdala)	0.3	0.3
Brain (cerebellum)	0.1	0.0
Brain (hippocampus)	0.7	0.8
Brain (thalamus)	0.4	0.6
Cerebral Cortex	0.3	0.8
Spinal cord	0.6	0.1
CNS ca. (glio/astro) U87-MG	0.0	0.0
CNS ca. (glio/astro) U-118-MG	0.0	0.0
CNS ca. (astro) SW1783	0.0	0.0
CNS ca.* (neuro; met) SK-N-AS	0.0	0.0
CNS ca. (astro) SF-539	0.0	0.0
CNS ca. (astro) SNB-75	0.0	0.0
CNS ca. (glio) SNB-19	0.0	0.0
CNS ca. (glio) U251	0.2	0.1
CNS ca. (glio) SF-295	0.0	0.1
Heart	17.0	50.3
Skeletal Muscle (new lot*)	16.0	18.2
Bone marrow	1.4	2.7
Thymus	2.8	0.9
Spleen	30.8	29.1

Lymph node	14.4	2.7
Colorectal	1.1	2.3
Stomach	33.2	11.5
Small intestine	41.5	52.5
Colon ca. SW480	0.0	0.0
Colon ca.* (SW480 met)SW620	0.0	0.0
Colon ca. HT29	0.0	0.0
Colon ca. HCT-116	0.0	0.0
Colon ca. CaCo-2	0.0	0.0
83219 CC Well to Mod Diff (ODO3866)	1.4	1.7
Colon ca. HCC-2998	0.0	0.0
Gastric ca.* (liver met) NCI-N87	0.7	0.9
Bladder	13.1	52.5
Trachea	9.6	2.1
Kidney	22.4	100.0
Kidney (fetal)	31.9	23.8
Renal ca. 786-0	0.0	0.0
Renal ca. A498	0.1	0.0
Renal ca. RXF 393	0.0	0.0
Renal ca. ACHN	0.0	0.0
Renal ca. UO-31	0.0	0.0
Renal ca. TK-10	0.0	0.0
Liver	1.6	2.1
Liver (fetal)	4.0	4.4
Liver ca. (hepatoblast) HepG2	0.0	0.0
Lung	4.1	1.0
Lung (fetal)	2.1	0.3
Lung ca. (small cell) LX-1	0.0	0.0
Lung ca. (small cell) NCI-H69	0.0	0.0
Lung ca. (s.cell var.) SHP-77	0.0	0.0
Lung ca. (large cell)NCI-H460	0.0	0.0
Lung ca. (non-sm. cell) A549	0.0	0.0
Lung ca. (non-s.cell) NCI-H23	0.0	0.0
Lung ca (non-s.cell) HOP-62	0.0	0.0
Lung ca. (non-s.cl) NCI-H522	0.0	0.0
Lung ca. (squam.) SW 900	0.0	0.0
Lung ca. (squam.) NCI-H596	0.0	0.0
Mammary gland	19.3	14.8
Breast ca.* (pl. effusion) MCF-7	0.0	0.0
Breast ca.* (pl.ef) MDA-MB-231	0.0	0.0
Breast ca.* (pl. effusion) T47D	0.0	0.0
Breast ca. BT-549	0.0	0.0
Breast ca. MDA-N	1.2	2.2
Ovary	0.8	3.0
Ovarian ca. OVCAR-3	0.0	0.0

Ovarian ca. OVCAR-4	0.0	0.0
Ovarian ca. OVCAR-5	0.1	0.1
Ovarian ca. OVCAR-8	0.0	0.2
Ovarian ca. IGROV-1	0.0	0.0
Ovarian ca.* (ascites) SK-OV-3	0.0	0.0
Uterus	12.8	9.2
Placenta	7.3	3.1
Prostate	12.3	19.5
Prostate ca.* (bone met)PC-3	0.0	0.0
Testis	1.4	0.2
Melanoma Hs688(A).T	0.0	0.0
Melanoma* (met) Hs688(B).T	0.0	0.0
Melanoma UACC-62	0.0	0.0
Melanoma M14	0.0	0.0
Melanoma LOX IMVI	0.0	0.0
Melanoma* (met) SK-MEL-5	0.0	0.0

Table 43. Panel 1.3D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	1.3dx4tm5483t ag760 b2		1.3dx4tm5483t ag760 b2
Liver adenocarcinoma	0.0	Kidney (fetal)	33.4
Pancreas	43.7	Renal ca. 786-0	0.0
Pancreatic ca. CAPAN 2	0.0	Renal ca. A498	0.2
Adrenal gland	21.5	Renal ca. RXF 393	0.0
Thyroid	79.7	Renal ca. ACHN	0.0
Salivary gland	13.9	Renal ca. UO-31	0.0
Pituitary gland	13.4	Renal ca. TK-10	0.0
Brain (fetal)	0.7	Liver	1.9
Brain (whole)	0.9	Liver (fetal)	12.4
Brain (amygdala)	1.6	Liver ca. (hepatoblast) HepG2	0.0
Brain (cerebellum)	0.4	Lung	15.3
Brain (hippocampus)	1.8	Lung (fetal)	6.1
Brain (substantia nigra)	2.3	Lung ca. (small cell) LX-1	0.0
Brain (thalamus)	2.7	Lung ca. (small cell) NCI-H69	0.0
Cerebral Cortex	0.7	Lung ca. (s.cell var.) SHP-77	0.0
Spinal cord	1.7	Lung ca. (large cell)NCI-H460	0.4
CNS ca. (glio/astro) U87-MG	0.0	Lung ca. (non-sm. cell) A549	0.0
CNS ca. (glio/astro) U-118-MG	0.0	Lung ca. (non-s.cell) NCI-H23	0.0
CNS ca. (astro) SW1783	0.0	Lung ca. (non-s.cell) HOP-62	0.0
CNS ca.* (neuro; met) SK-N-AS	0.0	Lung ca. (non-s.cl) NCI-H522	0.0
CNS ca. (astro) SF-539	0.0	Lung ca. (squam.) SW 900	0.0

CNS ca. (astro) SNB-75	0.0	Lung ca. (squam.) NCI-H596	0.0
CNS ca. (glio) SNB-19	0.0	Mammary gland	26.7
CNS ca. (glio) U251	0.7	Breast ca.* (pl. effusion) MCF-7	0.0
CNS ca. (glio) SF-295	0.0	Breast ca.* (pl. effusion) MDA-MB-231	0.0
Heart (fetal)	6.9	Breast ca.* (pl. effusion) T47D	0.0
Heart	10.9	Breast ca. BT-549	0.0
Fetal Skeletal	19.4	Breast ca. MDA-N	0.2
Skeletal muscle	9.9	Ovary	1.8
Bone marrow	7.8	Ovarian ca. OVCAR-3	0.0
Thymus	6.9	Ovarian ca. OVCAR-4	0.0
Spleen	90.4	Ovarian ca. OVCAR-5	0.0
Lymph node	73.5	Ovarian ca. OVCAR-8	0.0
Colorectal	7.9	Ovarian ca. IGROV-1	0.0
Stomach	65.6	Ovarian ca.* (ascites) SK-OV-3	0.0
Small intestine	100.0	Uterus	87.5
Colon ca. SW480	0.0	Placenta	6.4
Colon ca.* (SW480 met) SW620	0.0	Prostate	11.3
Colon ca. HT29	0.0	Prostate ca.* (bone met) PC-3	0.0
Colon ca. HCT-116	0.0	Testis	2.1
Colon ca. CaCo-2	0.0	Melanoma Hs688(A).T	0.0
83219 CC Well to Mod Diff (ODO3866)	24.0	Melanoma* (met) Hs688(B).T	0.0
Colon ca. HCC-2998	0.0	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87	1.7	Melanoma M14	0.0
Bladder	17.0	Melanoma LOX IMVI	0.0
Trachea	26.9	Melanoma* (met) SK-MEL-5	0.0
Kidney	18.2	Adipose	26.6

Table 44. Panel 2D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	2dtm2348f_ag1537		2dtm2348f_ag1537
Normal Colon GENPAK 061003	12.3	Kidney NAT Clontech 8120608	23.5
83219 CC Well to Mod Diff (ODO3866)	10.7	Kidney Cancer Clontech 8120613	21.5
83220 CC NAT (ODO3866)	12.2	Kidney NAT Clontech 8120614	12.3
83221 CC Gr.2 rectosigmoid (ODO3868)	3.2	Kidney Cancer Clontech 9010320	34.4
83222 CC NAT (ODO3868)	0.8	Kidney NAT Clontech 9010321	27.7
83235 CC Mod Diff (ODO3920)	3.4	Normal Uterus GENPAK 061018	9.3

83236 CC NAT (ODO3920)	2.2	Uterus Cancer GENPAK 064011	6.4
83237 CC Gr.2 ascend colon (ODO3921)	13.4	Normal Thyroid Clontech A+ 6570-1	84.1
83238 CC NAT (ODO3921)	5.8	Thyroid Cancer GENPAK 064010	20.6
83241 CC from Partial Hepatectomy (ODO4309)	9.6	Thyroid Cancer INVITROGEN A302152	15.2
83242 Liver NAT (ODO4309)	0.6	Thyroid NAT INVITROGEN A302153	21.3
87472 Colon mets to lung (OD04451-01)	5.5	Normal Breast GENPAK 061019	22.1
87473 Lung NAT (OD04451-02)	0.8	84877 Breast Cancer (OD04566)	8.4
Normal Prostate Clontech A+ 6546-1	14.1	85975 Breast Cancer (OD04590-01)	21.0
84140 Prostate Cancer (OD04410)	8.8	85976 Breast Cancer Mets (OD04590-03)	27.7
84141 Prostate NAT (OD04410)	6.9	87070 Breast Cancer Metastasis (OD04655-05)	9.1
87073 Prostate Cancer (OD04720-01)	3.1	GENPAK Breast Cancer 064006	10.1
87074 Prostate NAT (OD04720-02)	10.3	Breast Cancer Res. Gen. 1024	7.1
Normal Lung GENPAK 061010	11.8	Breast Cancer Clontech 9100266	10.4
83239 Lung Met to Muscle (ODO4286)	6.4	Breast NAT Clontech 9100265	7.4
83240 Muscle NAT (ODO4286)	9.9	Breast Cancer INVITROGEN A209073	27.4
84136 Lung Malignant Cancer (OD03126)	19.3	Breast NAT INVITROGEN A2090734	8.7
84137 Lung NAT (OD03126)	3.3	Normal Liver GENPAK 061009	1.1
84871 Lung Cancer (OD04404)	5.2	Liver Cancer GENPAK 064003	6.5
84872 Lung NAT (OD04404)	25.3	Liver Cancer Research Genetics RNA 1025	0.7
84875 Lung Cancer (OD04565)	3.4	Liver Cancer Research Genetics RNA 1026	8.1
84876 Lung NAT (OD04565)	3.1	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	1.9
85950 Lung Cancer (OD04237-01)	11.0	Paired Liver Tissue Research Genetics RNA 6004-N	3.6
85970 Lung NAT (OD04237-02)	18.2	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	9.3
83255 Ocular Mel Met to Liver (ODO4310)	0.7	Paired Liver Tissue Research Genetics RNA 6005-N	0.6
83256 Liver NAT (ODO4310)	1.7	Normal Bladder GENPAK 061001	14.1
84139 Melanoma Mets to Lung (OD04321)	3.9	Bladder Cancer Research Genetics RNA 1023	4.4

84138 Lung NAT (OD04321)	3.7	Bladder Cancer INVITROGEN A302173	3.6
Normal Kidney GENPAK 061008	40.6	87071 Bladder Cancer (OD04718-01)	7.4
83786 Kidney Ca, Nuclear grade 2 (OD04338)	5.7	87072 Bladder Normal Adjacent (OD04718-03)	15.2
83787 Kidney NAT (OD04338)	11.1	Normal Ovary Res. Gen.	1.4
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	2.5	Ovarian Cancer GENPAK 064008	6.5
83789 Kidney NAT (OD04339)	17.6	87492 Ovary Cancer (OD04768-07)	1.6
83790 Kidney Ca, Clear cell type (OD04340)	100.0	87493 Ovary NAT (OD04768-08)	9.2
83791 Kidney NAT (OD04340)	22.7	Normal Stomach GENPAK 061017	13.5
83792 Kidney Ca, Nuclear grade 3 (OD04348)	55.1	Gastric Cancer Clontech 9060358	2.8
83793 Kidney NAT (OD04348)	19.9	NAT Stomach Clontech 9060359	12.6
87474 Kidney Cancer (OD04622-01)	25.0	Gastric Cancer Clontech 9060395	20.6
87475 Kidney NAT (OD04622-03)	7.4	NAT Stomach Clontech 9060394	7.5
85973 Kidney Cancer (OD04450-01)	1.3	Gastric Cancer Clontech 9060397	10.0
85974 Kidney NAT (OD04450-03)	9.2	NAT Stomach Clontech 9060396	3.2
Kidney Cancer Clontech 8120607	9.2	Gastric Cancer GENPAK 064005	6.7

Table 45. Panel 4D

Tissue Name	Relative Expression(%) 4Dtm2478t_ag760	Tissue Name	Relative Expression(%)
			4Dtm2478t_ag760
93768_Secondary Th1_anti-CD28/anti-CD3	0.0	93100_HUVEC (Endothelial)_IL-1b	3.4
93769_Secondary Th2_anti-CD28/anti-CD3	0.1	93779_HUVEC (Endothelial)_IFN gamma	36.6
93770_Secondary Tr1_anti-CD28/anti-CD3	0.0	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	4.0
93573_Secondary Th1_resting day 4-6 in IL-2	0.1	93101_HUVEC (Endothelial)_TNF alpha + IL4	3.4
93572_Secondary Th2_resting day 4-6 in IL-2	0.0	93781_HUVEC (Endothelial)_IL-11	5.5
93571_Secondary Tr1_resting day 4-6 in IL-2	0.0	93583_Lung Microvascular Endothelial Cells_none	47.0
93568_primary Th1_anti-CD28/anti-CD3	0.0	93584_Lung Microvascular Endothelial Cells_TNF α (4)	22.8

		ng/ml) and IL1b (1 ng/ml)	
93569_primary Th2_anti-CD28/anti-CD3	0.0	92662_Microvascular Dermal endothelium none	40.1
93570_primary Tr1_anti-CD28/anti-CD3	0.1	92663_Microvasular Dermal endothelium_TNF α (4 ng/ml) and IL1b (1 ng/ml)	17.9
93565_primary Th1_resting dy 4-6 in IL-2	0.0	93773_Bronchial epithelium_TNF α (4 ng/ml) and IL1b (1 ng/ml) **	0.0
93566_primary Th2_resting dy 4-6 in IL-2	0.0	93347_Small Airway Epithelium none	0.0
93567_primary Tr1_resting dy 4-6 in IL-2	0.0	93348_Small Airway Epithelium_TNF α (4 ng/ml) and IL1b (1 ng/ml)	0.0
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	0.6	92668_Coronery Artery SMC resting	0.0
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	0.2	92669_Coronery Artery SMC_TNF α (4 ng/ml) and IL1b (1 ng/ml)	0.0
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.0	93107 astrocytes resting	0.0
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0.0	93108 astrocytes_TNF α (4 ng/ml) and IL1b (1 ng/ml)	0.0
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.0	92666_KU-812 (Basophil) resting	24.3
93354_CD4 none	0.3	92667_KU-812 (Basophil) PMA/ionoycin	29.7
93252_Secondary Th1/Th2/Tr1 anti-CD95 CH11	0.0	93579_CCD1106 (Keratinocytes) none	0.0
93103_LAK cells resting	0.1	93580_CCD1106 (Keratinocytes)_TNF α and IFNg **	0.0
93788_LAK cells IL-2	0.1	93791_Liver Cirrhosis	19.5
93787_LAK cells IL-2+IL-12	0.0	93792_Lupus Kidney	34.4
93789_LAK cells IL-2+IFN gamma	1.0	93577_NCI-H292	0.0
93790_LAK cells IL-2+ IL-18	0.7	93358_NCI-H292 IL-4	0.0
93104_LAK cells_PMA/ionomycin and IL-18	0.0	93360_NCI-H292 IL-9	0.0
93578_NK Cells IL-2 resting	0.4	93359_NCI-H292 IL-13	0.0
93109_Mixed Lymphocyte Reaction Two Way MLR	3.5	93357_NCI-H292 IFN gamma	0.0
93110_Mixed Lymphocyte Reaction Two Way MLR	1.3	93777_HPAEC -	0.9
93111_Mixed Lymphocyte Reaction Two Way MLR	0.0	93778_HPAEC IL-1 beta/TNA alpha	0.7
93112_Mononuclear Cells (PBMCs) resting	0.1	93254_Normal Human Lung Fibroblast none	0.0
93113_Mononuclear Cells	0.0	93253_Normal Human Lung	0.0

(PBMCs)_PWM		Fibroblast_TNF _a (4 ng/ml) and IL-1 _b (1 ng/ml)	
93114_Mononuclear Cells (PBMCs)_PHA-L	0.1	93257_Normal Human Lung Fibroblast IL-4	0.0
93249_Ramos (B cell)_none	0.0	93256_Normal Human Lung Fibroblast IL-9	0.0
93250_Ramos (B cell)_ionomycin	0.1	93255_Normal Human Lung Fibroblast IL-13	0.0
93349_B lymphocytes_PWM	0.0	93258_Normal Human Lung Fibroblast IFN gamma	0.0
93350_B lymphocytes_CD40L and IL-4	0.3	93106_Dermal Fibroblasts CCD1070 resting	0.0
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0.0	93361_Dermal Fibroblasts CCD1070 TNF alpha 4 ng/ml	0.0
93248_EOL-1 (Eosinophil)_dbcAMP/PMA/ionomycin	0.0	93105_Dermal Fibroblasts CCD1070 IL-1 beta 1 ng/ml	0.1
93356_Dendritic Cells_none	0.0	93772_dermal fibroblast_IFN gamma	0.0
93355_Dendritic Cells_LPS 100 ng/ml	2.3	93771_dermal fibroblast IL-4	0.1
93775_Dendritic Cells_anti-CD40	0.0	93260_IBD Colitis 2	1.5
93774_Monocytes_resting	0.8	93261_IBD Crohns	9.0
93776_Monocytes_LPS 50 ng/ml	0.0	735010_Colon normal	40.3
93581_Macrophages_resting	0.0	735019_Lung none	100.0
93582_Macrophages_LPS 100 ng/ml	0.6	64028-1_Thymus none	95.3
93098_HUVEC (Endothelial)_none	3.8	64030-1_Kidney none	59.9
93099_HUVEC (Endothelial)_starved	16.8		

Panel 1.2 Summary: Ag760/Ag1537 Results from two experiments using different probe/primer sets show some differences. Using Ag760, expression of the NOV7a gene is high to moderate across many of the normal tissue samples on this panel with highest expression in thyroid (CT = 20.1). Using Ag1537, expression of the NOV7a gene is high to moderate across many of the normal tissue samples on this panel with highest expression in kidney (CT = 21.6). Although the level of expression in some of the samples varies between the experiments, it is clear that that this gene is exclusively expressed in samples derived from normal tissues and not in cancer cell lines. Thus, expression of this gene could be used to distinguish between normal tissues and cultured cells.

The PV-1-like protein is a plasma membrane protein with an extracellular domain. Expression of this gene is high (CT values less than or equal to 27) in a wide array of

metabolic tissues including pancreas, adrenal gland, thyroid, pituitary, adult and fetal heart, skeletal muscle and adult and fetal liver. The extracellular domain of this protein makes it a potential antibody target for the treatment of diseases in any or all of these tissues.

5 **Panel 1.3D Summary:** Ag760 Expression of the NOV7a gene is highest in small intestine (CT = 26). This gene is exclusively expressed in samples derived from normal tissues and not cancer cell lines, consistent with what is observed in Panel 1.2. Thus, the expression of this gene could be used to distinguish between normal tissues and cultured cells.

10 Among metabolic tissues expression is high in pancreas, adipose, adrenal gland, thyroid, pituitary gland, heart, skeletal muscle, and liver.

This gene is expressed at low to moderate levels throughout the CNS and is specifically found in amygdala, cerebellum, hippocampus, substantia nigra, thalamus, cerebral cortex and spinal cord.

15 **Panel 2D Summary:** Ag1537 Expression of the NOV7a gene is highest in a kidney cancer sample (CT = 25). Overall, this gene is widely expressed widely across Panel 2D in both normal and adjacent cancer tissue. However, in a couple of instances, it appears that the NOV7a gene is more highly expressed in kidney cancer tissue than in adjacent normal tissue. Therefore, this gene could be used to distinguish kidney cancers from normal kidney tissue. In 20 addition, therapeutic modulation of this gene, through the use of small molecule drugs or antibodies, might be of benefit in the treatment of kidney cancer.

25 **Panel 4D Summary:** Ag760 Expression of the NOV7a gene is highest in lung and thymus (CT = 26). High expression of this gene is also seen in normal kidney and colon with more moderate expression in endothelial cells and basophils. Expression of the NOV7a gene in lung and lung microvascular endothelial cells is consistent with the expression pattern observed for the PV-1 protein (1). Antibodies raised against the protein encoded by the NOV7a gene could prevent transendothelial trafficking of inflammatory cells to different tissues sites and therefore have a potential use for treatment of inflammatory diseases 30 including delayed type hypersensitivity, asthma, emphysema, rheumatoid arthritis and IBD.

References:

1. Stan R.V., Kubitz M., and Palade G.E. (1999) PV-1 is a component of the fenestral and stomatal diaphragms in fenestrated endothelia. Proc. Natl. Acad. Sci. USA 96:13203-13207.

5 PV-1 is a novel endothelial protein shown by immunocytochemical tests to be specifically associated with the stomatal diaphragms of caveolae in lung endothelium. Although the highest expression levels of both mRNA and protein are in the lung, PV-1 also has been found to be expressed in other organs. Using a specific antibody to the extracellular domain of PV-1, Stan et al. have extended the survey on the presence of this protein at light
10 and electron microscope level in several rat organs. Stan et al. show that by immunofluorescence the antibody recognizes with high specificity the endothelium of the fenestrated peritubular capillaries of the kidney and those of the intestinal villi, pancreas, and adrenals. By immunolocalization at electron microscope level, the antibody recognizes specifically the diaphragms of the fenestrae and the stomatal diaphragms of caveolae and
15 transendothelial channels in the endothelia of these vascular beds. No signal was detected in the continuous endothelium of the heart, skeletal muscle, intestinal muscularis, or brain capillaries or the nondiaphragmed fenestrated endothelium of kidney glomeruli. Taken together, these findings define the only antigen to be localized thus far in fenestral diaphragms. They also show that the stomatal diaphragms of caveolae and transendothelial
20 channels and the fenestral diaphragms might be biochemically related, in addition to being morphologically similar structures.

PMID: 10557298

25

NOV8a and NOV8b

Expression of gene NOV8a and its variant was assessed using the primer-probe sets
30 Ag147, Ag718, Ag3681, and Ag4085, described in Tables 46, 47, and 48. Results from RTQ-PCR runs are shown in Tables 49, 50, 51, 52, and 53.

Table 46. Probe Name Ag147

Primers	Sequences	TM	Length	Start	SEQ ID
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			Position	NO:
Forward	5'-TGAAGACAGCACCTCCCTATCA-3'	22	1411	118
Probe	FAM-5'- CGGCTCCGTGCTGTACCCAG-3'- TAMRA	21	1436	119
Reverse	5'-AAGAACCTCAGCATGCCATA-3'	22	1472	120

Table 47 Probe Name Ag718

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-AGAAGGAATCTCTGGGAAAGCT-3'	59.9	22	949	121
Probe	FAM-5'- CCACTGGAGATGCTTGTCTACCA-3'-TAMRA	68.6	27	973	122
Reverse	5'-GACAGAGCACTGGCTAGTCAC-3'	59.2	22	1003	123

5

Table 48. Probe Name Ag3681/Ag4085 (identical sequences)

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-GAATCATCCACAAGTCATCCAT-3'	58.7	22	5818	124
Probe	FAM-5'- CTCACTCCCACATCTCATGCCTCCCAG-3'-TAMRA	71.2	25	5841	125
Reverse	5'-CATGCTGAATGATCGTGACA-3'	59.2	20	5879	126

10

Table 49. Panel 1

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	tm289f		tm289f
Endothelial cells	0.0	Renal ca. 786-0	1.3
Endothelial cells (treated)	1.2	Renal ca. A498	0.4
Pancreas	1.6	Renal ca. RXF 393	0.4
Pancreatic ca. CAPAN 2	0.5	Renal ca. ACHN	1.1
Adrenal gland	3.0	Renal ca. UO-31	1.4
Thyroid	0.4	Renal ca. TK-10	0.8
Salavary gland	0.9	Liver	0.5
Pituitary gland	2.0	Liver (fetal)	0.2
Brain (fetal)	7.7	Liver ca. (hepatoblast) HepG2	0.2
Brain (whole)	45.1	Lung	7.6
Brain (amygdala)	8.0	Lung (fetal)	3.2
Brain (cerebellum)	49.0	Lung ca. (small cell) LX-1	0.2

Brain (hippocampus)	8.4	Lung ca. (small cell) NCI-H69	0.6
Brain (substantia nigra)	11.7	Lung ca. (s.cell var.) SHP-77	0.0
Brain (thalamus)	5.3	Lung ca. (large cell) NCI-H460	0.0
Brain (hypothalamus)	1.5	Lung ca. (non-sm. cell) A549	0.4
Spinal cord	5.6	Lung ca. (non-s.cell) NCI-H23	0.4
CNS ca. (glio/astro) U87-MG	0.2	Lung ca (non-s.cell) HOP-62	2.4
CNS ca. (glio/astro) U-118-MG	0.0	Lung ca. (non-s.cl) NCI-H522	0.9
CNS ca. (astro) SW1783	0.0	Lung ca. (squam.) SW 900	2.4
CNS ca.* (neuro; met) SK-N-AS	0.2	Lung ca. (squam.) NCI-H596	0.1
CNS ca. (astro) SF-539	0.8	Mammary gland	15.6
CNS ca. (astro) SNB-75	0.8	Breast ca.* (pl. effusion) MCF-7	0.8
CNS ca. (glio) SNB-19	8.6	Breast ca.* (pl.ef) MDA-MB-231	0.4
CNS ca. (glio) U251	0.7	Breast ca.* (pl. effusion) T47D	10.7
CNS ca. (glio) SF-295	3.6	Breast ca. BT-549	0.0
Heart	11.3	Breast ca. MDA-N	0.3
Skeletal muscle	1.6	Ovary	8.1
Bone marrow	0.3	Ovarian ca. OVCAR-3	0.7
Thymus	6.4	Ovarian ca. OVCAR-4	4.7
Spleen	0.5	Ovarian ca. OVCAR-5	1.3
Lymph node	1.2	Ovarian ca. OVCAR-8	1.3
Colon (ascending)	1.6	Ovarian ca. IGROV-1	0.5
Stomach	5.9	Ovarian ca.* (ascites) SK-OV-3	1.3
Small intestine	1.7	Uterus	9.0
Colon ca. SW480	2.4	Placenta	32.1
Colon ca.* (SW480 met)SW620	0.2	Prostate	1.9
Colon ca. HT29	0.2	Prostate ca.* (bone met)PC-3	0.0
Colon ca. HCT-116	0.0	Testis	100.0
Colon ca. CaCo-2	1.1	Melanoma Hs688(A).T	0.2
Colon ca. HCT-15	0.7	Melanoma* (met) Hs688(B).T	0.2
Colon ca. HCC-2998	1.5	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87	11.4	Melanoma M14	0.1
Bladder	2.3	Melanoma LOX IMVI	0.2
Trachea	3.2	Melanoma* (met) SK-MEL-5	0.0
Kidney	6.7	Melanoma SK-MEL-28	0.1
Kidney (fetal)	6.1		

Table 50. Panel 1.2

Tissue Name	Relative Expression(%)		
	1.2tm888f_ag718	1.2tm1997f_ag718	1.2tm2041f_ag718
Endothelial cells	0.6	0.4	0.2

Heart (fetal)	7.4	10.2	8.1
Pancreas	14.8	0.1	0.0
Pancreatic ca. CAPAN 2	0.0	0.0	0.0
Adrenal Gland (new lot*)	5.4	4.0	4.3
Thyroid	3.8	0.0	0.0
Salavary gland	4.0	1.9	1.4
Pituitary gland	19.2	0.4	0.2
Brain (fetal)	41.8	1.3	1.5
Brain (whole)	37.6	1.6	3.5
Brain (amygdala)	16.3	7.1	5.5
Brain (cerebellum)	17.3	1.8	1.6
Brain (hippocampus)	26.6	16.6	16.2
Brain (thalamus)	14.5	6.7	9.3
Cerebral Cortex	79.6	81.8	100.0
Spinal cord	15.0	0.7	0.9
CNS ca. (glio/astro) U87-MG	0.0	0.0	0.0
CNS ca. (glio/astro) U-118-MG	0.0	0.0	0.0
CNS ca. (astro) SW1783	0.0	0.0	0.0
CNS ca.* (neuro; met) SK-N-AS	2.9	0.4	0.4
CNS ca. (astro) SF-539	2.4	1.2	1.0
CNS ca. (astro) SNB-75	0.7	0.4	0.2
CNS ca. (glio) SNB-19	27.2	7.2	5.8
CNS ca. (glio) U251	4.6	0.6	0.9
CNS ca. (glio) SF-295	7.2	7.4	5.0
Heart	73.7	100.0	79.0
Skeletal Muscle (new lot*)	36.9	17.3	15.3
Bone marrow	0.6	0.2	0.2
Thymus	1.7	0.1	0.0
Spleen	0.6	0.2	0.1
Lymph node	1.9	0.0	0.0
Colorectal	0.7	0.8	0.9
Stomach	8.4	0.3	0.6
Small intestine	4.3	1.9	1.8
Colon ca. SW480	10.2	4.3	4.1
Colon ca.* (SW480 met)SW620	0.3	0.0	0.0
Colon ca. HT29	0.0	0.0	0.0
Colon ca. HCT-116	0.1	0.1	0.0
Colon ca. CaCo-2	1.4	0.5	0.4
83219 CC Well to Mod Diff (ODO3866)	0.3	0.3	0.3
Colon ca. HCC-2998	1.4	1.4	1.2
Gastric ca.* (liver met) NCI-N87	35.4	15.8	8.7
Bladder	6.2	4.6	3.7
Trachea	4.2	0.3	0.2
Kidney	16.7	46.7	48.0
Kidney (fetal)	20.2	2.8	2.9
Renal ca. 786-0	1.7	0.9	0.9
Renal ca. A498	0.2	0.1	0.1
Renal ca. RXF 393	0.4	0.1	0.2

Renal ca. ACHN	2.9	3.1	1.9
Renal ca. UO-31	1.5	1.4	1.2
Renal ca. TK-10	0.5	0.4	0.2
Liver	1.6	0.6	0.5
Liver (fetal)	1.1	0.4	0.5
Liver ca. (hepatoblast) HepG2	0.1	0.3	0.0
Lung	12.8	0.4	0.6
Lung (fetal)	9.6	0.5	0.6
Lung ca. (small cell) LX-1	0.3	0.2	0.2
Lung ca. (small cell) NCI-H69	0.9	0.6	0.4
Lung ca. (s.cell var.) SHP-77	0.3	0.0	0.0
Lung ca. (large cell) NCI-H460	0.2	0.2	2.7
Lung ca. (non-sm. cell) A549	0.3	0.2	0.2
Lung ca. (non-s.cell) NCI-H23	0.6	0.7	0.4
Lung ca (non-s.cell) HOP-62	5.0	4.6	0.6
Lung ca. (non-s.cl) NCI-H522	1.0	1.2	0.5
Lung ca. (squam.) SW 900	2.4	2.6	2.0
Lung ca. (squam.) NCI-H596	0.3	0.1	0.0
Mammary gland	13.4	2.1	3.0
Breast ca.* (pl. effusion) MCF-7	0.2	0.0	0.0
Breast ca.* (pl.ef) MDA-MB-231	2.1	0.9	0.4
Breast ca.* (pl. effusion) T47D	14.5	9.5	8.7
Breast ca. BT-549	1.4	0.5	0.5
Breast ca. MDA-N	0.2	0.1	0.0
Ovary	19.1	18.9	13.6
Ovarian ca. OVCAR-3	6.7	3.0	2.9
Ovarian ca. OVCAR-4	17.8	19.6	17.2
Ovarian ca. OVCAR-5	3.3	2.8	2.1
Ovarian ca. OVCAR-8	1.4	1.5	1.0
Ovarian ca. IGROV-1	1.8	1.3	0.8
Ovarian ca.* (ascites) SK-OV-3	10.3	5.1	6.4
Uterus	7.0	1.8	1.4
Placenta	100.0	3.1	3.9
Prostate	4.0	2.8	1.4
Prostate ca.* (bone met)PC-3	7.7	5.4	4.4
Testis	45.7	1.5	1.3
Melanoma Hs688(A).T	0.0	0.0	0.0
Melanoma* (met) Hs688(B).T	0.1	0.0	0.0
Melanoma UACC-62	0.5	0.2	0.2
Melanoma M14	0.1	0.2	0.0
Melanoma LOX IMVI	0.0	0.0	0.0
Melanoma* (met) SK-MEL-5	0.2	0.1	0.2

Table 51. Panel 2D

Tissue Name	Relative Expression(%)
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	2dtm2721f_ag718	2Dtm2831f_ag718
Normal Colon GENPAK 061003	13.6	15.9
83219 CC Well to Mod Diff (ODO3866)	0.9	2.0
83220 CC NAT (ODO3866)	1.7	1.5
83221 CC Gr.2 rectosigmoid (ODO3868)	3.4	3.2
83222 CC NAT (ODO3868)	2.6	2.6
83235 CC Mod Diff (ODO3920)	2.4	3.0
83236 CC NAT (ODO3920)	2.9	3.1
83237 CC Gr.2 ascend colon (ODO3921)	6.5	9.1
83238 CC NAT (ODO3921)	1.3	1.2
83241 CC from Partial Hepatectomy (ODO4309)	1.3	0.7
83242 Liver NAT (ODO4309)	1.3	1.5
87472 Colon mets to lung (OD04451-01)	4.5	4.9
87473 Lung NAT (OD04451-02)	26.8	29.7
Normal Prostate Clontech A+ 6546-1	5.2	5.6
84140 Prostate Cancer (OD04410)	12.6	11.3
84141 Prostate NAT (OD04410)	10.6	16.4
87073 Prostate Cancer (OD04720-01)	19.6	19.3
87074 Prostate NAT (OD04720-02)	14.7	16.4
Normal Lung GENPAK 061010	53.6	56.6
83239 Lung Met to Muscle (ODO4286)	0.5	0.5
83240 Muscle NAT (ODO4286)	3.6	5.5
84136 Lung Malignant Cancer (OD03126)	22.5	18.9
84137 Lung NAT (OD03126)	73.2	79.6
84871 Lung Cancer (OD04404)	9.9	10.9
84872 Lung NAT (OD04404)	29.9	31.2
84875 Lung Cancer (OD04565)	3.3	5.8
84876 Lung NAT (OD04565)	50.0	47.0
85950 Lung Cancer (OD04237-01)	4.6	3.0
85970 Lung NAT (OD04237-02)	28.3	39.2
83255 Ocular Mel Met to Liver (ODO4310)	1.6	0.6
83256 Liver NAT (ODO4310)	0.3	0.7
84139 Melanoma Mets to Lung (OD04321)	0.6	1.3
84138 Lung NAT (OD04321)	48.6	57.0
Normal Kidney GENPAK 061008	59.9	63.7
83786 Kidney Ca, Nuclear grade 2 (OD04338)	2.4	4.2
83787 Kidney NAT (OD04338)	21.6	23.3
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	2.0	2.4
83789 Kidney NAT (OD04339)	68.8	70.7
83790 Kidney Ca, Clear cell type (OD04340)	100.0	100.0
83791 Kidney NAT (OD04340)	59.0	65.1
83792 Kidney Ca, Nuclear grade 3 (OD04348)	3.9	4.0
83793 Kidney NAT (OD04348)	34.9	29.9
87474 Kidney Cancer (OD04622-01)	6.0	12.0

87475 Kidney NAT (OD04622-03)	8.1	8.7
85973 Kidney Cancer (OD04450-01)	0.8	1.4
85974 Kidney NAT (OD04450-03)	26.2	25.5
Kidney Cancer Clontech 8120607	1.1	0.4
Kidney NAT Clontech 8120608	18.6	20.6
Kidney Cancer Clontech 8120613	3.5	3.4
Kidney NAT Clontech 8120614	52.8	54.0
Kidney Cancer Clontech 9010320	10.3	9.9
Kidney NAT Clontech 9010321	34.2	31.0
Normal Uterus GENPAK 061018	7.1	4.5
Uterus Cancer GENPAK 064011	12.9	11.8
Normal Thyroid Clontech A+ 6570-1	2.5	1.8
Thyroid Cancer GENPAK 064010	1.5	1.8
Thyroid Cancer INVITROGEN A302152	3.5	3.4
Thyroid NAT INVITROGEN A302153	2.3	2.7
Normal Breast GENPAK 061019	27.5	26.6
84877 Breast Cancer (OD04566)	6.2	11.7
85975 Breast Cancer (OD04590-01)	7.5	6.2
85976 Breast Cancer Mets (OD04590-03)	21.2	24.5
87070 Breast Cancer Metastasis (OD04655-05)	4.6	5.8
GENPAK Breast Cancer 064006	15.8	18.6
Breast Cancer Res. Gen. 1024	29.7	26.4
Breast Cancer Clontech 9100266	2.4	3.6
Breast NAT Clontech 9100265	6.5	6.2
Breast Cancer INVITROGEN A209073	22.5	24.7
Breast NAT INVITROGEN A2090734	15.1	18.4
Normal Liver GENPAK 061009	0.7	0.7
Liver Cancer GENPAK 064003	1.6	1.3
Liver Cancer Research Genetics RNA 1025	1.6	1.9
Liver Cancer Research Genetics RNA 1026	1.8	1.2
Paired Liver Cancer Tissue Research Genetics RNA 6004-T	0.8	1.6
Paired Liver Tissue Research Genetics RNA 6004-N	0.8	1.4
Paired Liver Cancer Tissue Research Genetics RNA 6005-T	1.3	1.0
Paired Liver Tissue Research Genetics RNA 6005-N	0.0	0.0
Normal Bladder GENPAK 061001	7.0	3.9
Bladder Cancer Research Genetics RNA 1023	1.0	1.6
Bladder Cancer INVITROGEN A302173	12.9	16.8
87071 Bladder Cancer (OD04718-01)	16.7	21.8
87072 Bladder Normal Adjacent (OD04718-03)	4.7	4.8
Normal Ovary Res. Gen.	13.7	15.3
Ovarian Cancer GENPAK 064008	37.6	46.3
87492 Ovary Cancer (OD04768-07)	24.5	22.8
87493 Ovary NAT (OD04768-08)	3.6	4.4
Normal Stomach GENPAK 061017	14.2	16.2
Gastric Cancer Clontech 9060358	4.6	5.5

NAT Stomach Clontech 9060359	2.2	3.3
Gastric Cancer Clontech 9060395	3.2	3.0
NAT Stomach Clontech 9060394	2.8	2.0
Gastric Cancer Clontech 9060397	4.6	4.7
NAT Stomach Clontech 9060396	1.0	2.3
Gastric Cancer GENPAK 064005	5.3	5.3

Table 52. Panel 4D/4R

Tissue Name	Relative Expression(%)		
	4Dtm1839f_ag718	4Dtm1909f_ag718	4rtm2719f_ag718
93768 Secondary Th1 anti-CD28/anti-CD3	0.0	0.3	0.0
93769 Secondary Th2 anti-CD28/anti-CD3	0.1	0.1	0.5
93770 Secondary Tr1 anti-CD28/anti-CD3	0.6	0.0	0.9
93573 Secondary Th1 resting day 4-6 in IL-2	0.0	0.2	0.3
93572 Secondary Th2 resting day 4-6 in IL-2	0.2	0.3	0.1
93571 Secondary Tr1 resting day 4-6 in IL-2	0.1	0.2	0.8
93568 primary Th1 anti-CD28/anti-CD3	0.5	0.2	0.3
93569 primary Th2 anti-CD28/anti-CD3	0.3	0.3	0.3
93570 primary Tr1 anti-CD28/anti-CD3	0.6	0.5	0.0
93565 primary Th1 resting dy 4-6 in IL-2	1.0	0.3	2.3
93566 primary Th2 resting dy 4-6 in IL-2	0.2	0.4	0.0
93567 primary Tr1 resting dy 4-6 in IL-2	0.2	0.0	0.0
93351_CD45RA CD4 lymphocyte anti-CD28/anti-CD3	0.2	0.4	0.4
93352_CD45RO CD4 lymphocyte anti-CD28/anti-CD3	0.2	0.0	1.2
93251_CD8 Lymphocytes anti-CD28/anti-CD3	0.4	0.3	0.6
93353_chronic CD8 Lymphocytes 2ry resting dy 4-6 in IL-2	0.4	0.7	0.8
93574_chronic CD8 Lymphocytes 2ry activated CD3/CD28	0.2	0.1	0.0
93354 CD4 none	0.9	0.5	0.9
93252_Secondary Th1/Th2/Tr1 anti-CD95 CH11	0.4	0.3	0.0
93103_LAK cells resting	0.2	0.3	0.5
93788_LAK cells IL-2	0.4	0.3	0.7
93787_LAK cells IL-2+IL-12	0.0	0.2	0.0
93789_LAK cells IL-2+IFN gamma	0.3	0.6	1.0
93790_LAK cells IL-2+ IL-18	0.3	0.3	0.6
93104_LAK cells PMA/ionomycin and IL-18	0.2	0.1	0.0
93578_NK Cells IL-2 resting	0.0	0.7	0.8
93109_Mixed Lymphocyte Reaction_Two Way MLR	0.1	0.5	0.0

93110_Mixed Lymphocyte Reaction_Two Way MLR	0.2	0.2	0.0
93111_Mixed Lymphocyte Reaction_Two Way MLR	0.0	0.2	0.0
93112_Mononuclear Cells (PBMCs) resting	0.2	0.2	0.0
93113_Mononuclear Cells (PBMCs) PWM	0.9	0.9	1.5
93114_Mononuclear Cells (PBMCs) PHA-L	0.5	0.3	0.4
93249_Ramos (B cell) none	0.3	0.2	0.9
93250_Ramos (B cell) ionomycin	0.3	0.0	0.8
93349_B lymphocytes PWM	0.5	0.3	1.5
93350_B lymphocytes_CD40L and IL-4	1.2	0.9	1.2
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0.1	0.0	0.0
93248_EOL-1 (Eosinophil) dbcAMP/PMA/ionomycin	0.4	1.0	1.5
93356_Dendritic Cells none	0.5	0.3	0.3
93355_Dendritic Cells LPS 100 ng/ml	0.0	0.3	0.0
93775_Dendritic Cells anti-CD40	0.1	0.2	0.0
93774_Monocytes resting	0.3	0.0	0.4
93776_Monocytes LPS 50 ng/ml	0.6	0.5	0.0
93581_Macrophages resting	0.2	0.4	0.0
93582_Macrophages LPS 100 ng/ml	0.2	0.2	0.0
93098_HUVEC (Endothelial) none	1.4	1.5	2.1
93099_HUVEC (Endothelial) starved	5.0	3.7	10.3
93100_HUVEC (Endothelial) IL-1b	3.9	3.4	21.6
93779_HUVEC (Endothelial) IFN gamma	0.6	0.7	1.7
93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	4.5	5.5	8.1
93101_HUVEC (Endothelial)_TNF alpha + IL4	4.4	4.4	6.4
93781_HUVEC (Endothelial) IL-11	0.8	0.6	1.3
93583_Lung Microvascular Endothelial Cells none	6.2	5.4	8.8
93584_Lung Microvascular Endothelial Cells TNFa (4 ng/ml) and IL1b (1 ng/ml)	10.2	7.4	40.3
92662_Microvascular Dermal endothelium none	17.0	17.1	9.0
92663_Microvasular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	27.9	22.2	53.6
93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	12.1	15.4	17.6
93347_Small Airway Epithelium none	2.2	3.8	6.9
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	36.9	28.9	63.7
92668_Coronery Artery SMC resting	0.4	0.2	0.9
92669_Coronery Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.2	0.0	0.3
93107_astrocytes resting	0.3	0.5	0.8

93108_astrocytes_TNF α (4 ng/ml) and IL1 β (1 ng/ml)	4.0	2.3	6.5
92666_KU-812 (Basophil) resting	0.2	0.4	0.3
92667_KU-812 (Basophil) PMA/ionoycin	0.2	0.3	0.0
93579_CCD1106 (Keratinocytes) none	6.2	5.7	10.4
93580_CCD1106 (Keratinocytes)_TNF α and IFNg **	100.0	100.0	30.6
93791_Liver Cirrhosis	1.3	0.7	6.2
93792_Lupus Kidney	14.9	11.5	25.2
93577_NCI-H292	13.7	12.2	25.0
93358_NCI-H292 IL-4	24.7	23.8	100.0
93360_NCI-H292 IL-9	13.8	10.7	28.9
93359_NCI-H292 IL-13	9.5	12.0	12.7
93357_NCI-H292 IFN gamma	8.5	10.0	15.7
93777_HPAEC -	0.8	1.3	2.3
93778_HPAEC IL-1 beta/TNF α	8.7	11.0	11.7
93254_Normal Human Lung Fibroblast none	0.3	0.2	0.0
93253_Normal Human Lung Fibroblast TNF α (4 ng/ml) and IL-1 β (1 ng/ml)	0.2	0.5	0.3
93257_Normal Human Lung Fibroblast IL-4	0.2	0.0	1.8
93256_Normal Human Lung Fibroblast IL-9	0.0	0.2	0.7
93255_Normal Human Lung Fibroblast IL-13	0.2	0.1	0.0
93258_Normal Human Lung Fibroblast IFN gamma	0.4	0.0	0.5
93106_Dermal Fibroblasts CCD1070 resting	0.4	0.8	0.3
93361_Dermal Fibroblasts CCD1070 TNF α 4 ng/ml	0.9	0.5	0.8
93105_Dermal Fibroblasts CCD1070 IL-1 beta 1 ng/ml	0.3	0.7	0.3
93772_dermal fibroblast IFN gamma	0.2	0.0	0.0
93771_dermal fibroblast IL-4	0.1	0.2	0.0
93260_IBD Colitis 2	0.1	0.3	0.3
93261_IBD Crohns	0.3	0.5	1.7
735010_Colon normal	1.6	2.8	5.6
735019_Lung none	18.9	21.8	51.0
64028-1_Thymus none	88.3	88.9	96.6
64030-1_Kidney none	6.8	8.0	15.7

Table 53. Panel 4.1D

Tissue Name	Relative Expression(%)	Relative Expression(%)
	4.1dx4tm5977f_ag3681_b1	4.1dtm6217f_ag4085
93768_Secondary Th1 anti-CD28/anti-CD3	1.9	3.0
93769_Secondary Th2 anti-CD28/anti-CD3	4.0	2.2

93770 Secondary Tr1 anti-CD28/anti-CD3	3.5	2.5
93573 Secondary Th1 resting day 4-6 in IL-2	1.9	2.0
93572 Secondary Th2 resting day 4-6 in IL-2	4.1	0.0
93571 Secondary Tr1 resting day 4-6 in IL-2	2.5	2.2
93568 primary Th1 anti-CD28/anti-CD3	2.0	5.1
93569 primary Th2 anti-CD28/anti-CD3	3.5	1.8
93570 primary Tr1 anti-CD28/anti-CD3	2.4	5.4
93565 primary Th1 resting dy 4-6 in IL-2	0.5	1.6
93566 primary Th2 resting dy 4-6 in IL-2	1.9	0.0
93567 primary Tr1 resting dy 4-6 in IL-2	4.1	0.0
93351 CD45RA CD4 lymphocyte anti-CD28/anti-CD3	3.5	1.7
93352 CD45RO CD4 lymphocyte anti-CD28/anti-CD3	3.3	1.9
93251 CD8 Lymphocytes anti-CD28/anti-CD3	2.6	1.4
93353 chronic CD8 Lymphocytes 2ry resting dy 4-6 in IL-2	3.6	0.9
93574 chronic CD8 Lymphocytes 2ry activated CD3/CD28	1.1	1.3
93354 CD4 none	2.6	2.7
93252 Secondary Th1/Th2/Tr1 anti-CD95 CH11	2.0	0.9
93103 LAK cells resting	2.0	1.4
93788 LAK cells IL-2	1.6	1.3
93787 LAK cells IL-2+IL-12	1.9	1.1
93789 LAK cells IL-2+IFN gamma	2.8	0.0
93790 LAK cells IL-2+ IL-18	2.4	0.0
93104 LAK cells PMA/ionomycin and IL-18	1.7	1.1
93578 NK Cells IL-2 resting	3.1	2.5
93109 Mixed Lymphocyte Reaction Two Way MLR	2.6	3.3
93110 Mixed Lymphocyte Reaction Two Way MLR	0.8	0.0
93111 Mixed Lymphocyte Reaction Two Way MLR	1.4	1.8
93112 Mononuclear Cells (PBMCs) resting	1.8	1.2
93113 Mononuclear Cells (PBMCs) PWM	1.2	1.4
93114 Mononuclear Cells (PBMCs) PHA-L	1.7	0.0
93249 Ramos (B cell) none	1.0	0.9
93250 Ramos (B cell) ionomycin	0.0	0.0
93349 B lymphocytes PWM	0.3	0.8
93350 B lymphocytes CD40L and IL-4	4.1	4.3
92665 EOL-1 (Eosinophil) dbcAMP differentiated	5.6	2.6
93248 EOL-1 (Eosinophil) dbcAMP/PMAionomycin	7.1	4.3
93356 Dendritic Cells none	1.8	3.4
93355 Dendritic Cells LPS 100 ng/ml	0.6	0.0
93775 Dendritic Cells anti-CD40	2.8	0.0
93774 Monocytes resting	2.4	2.2
93776 Monocytes LPS 50 ng/ml	3.7	5.5
93581 Macrophages resting	2.1	0.0
93582 Macrophages LPS 100 ng/ml	1.3	2.1
93098 HUVEC (Endothelial) none	4.7	6.1
93099 HUVEC (Endothelial) starved	6.8	5.5

93100 HUVEC (Endothelial) IL-1b	19.5	14.9
93779 HUVEC (Endothelial) IFN gamma	4.6	8.7
93102 HUVEC (Endothelial) TNF alpha + IFN gamma	24.8	32.1
93101 HUVEC (Endothelial) TNF alpha + IL4	14.4	13.3
93781 HUVEC (Endothelial) IL-11	2.9	5.0
93583 Lung Microvascular Endothelial Cells none	27.4	29.1
93584 Lung Microvascular Endothelial Cells TNFa (4 ng/ml) and IL1b (1 ng/ml)	60.1	44.4
92662 Microvascular Dermal endothelium none	20.6	18.8
92663 Microvasular Dermal endothelium TNFa (4 ng/ml) and IL1b (1 ng/ml)	48.3	47.6
93773 Bronchial epithelium TNFa (4 ng/ml) and IL1b (1 ng/ml) **	22.7	22.8
93347 Small Airway Epithelium none	6.4	6.9
93348 Small Airway Epithelium TNFa (4 ng/ml) and IL1b (1 ng/ml)	36.3	27.4
92668 Coronery Artery SMC resting	1.3	2.5
92669 Coronery Artery SMC TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.9	4.6
93107 astrocytes resting	5.2	4.8
93108 astrocytes TNFa (4 ng/ml) and IL1b (1 ng/ml)	7.5	13.3
92666 KU-812 (Basophil) resting	0.4	2.5
92667 KU-812 (Basophil) PMA/ionoycin	2.3	4.7
93579 CCD1106 (Keratinocytes) none	20.2	44.8
93580 CCD1106 (Keratinocytes) TNFa and IFNg **	53.3	85.9
93791 Liver Cirrhosis	6.7	2.8
93577 NCI-H292	19.9	18.3
93358 NCI-H292 IL-4	30.3	39.0
93360 NCI-H292 IL-9	15.2	18.8
93359 NCI-H292 IL-13	35.9	52.5
93357 NCI-H292 IFN gamma	32.2	33.7
93777 HPAEC -	6.7	12.9
93778 HPAEC IL-1 beta/TNA alpha	36.8	28.7
93254 Normal Human Lung Fibroblast none	1.2	4.0
93253 Normal Human Lung Fibroblast TNFa (4 ng/ml) and IL-1b (1 ng/ml)	1.1	2.4
93257 Normal Human Lung Fibroblast IL-4	2.4	0.0
93256 Normal Human Lung Fibroblast IL-9	1.2	1.5
93255 Normal Human Lung Fibroblast IL-13	0.4	2.4
93258 Normal Human Lung Fibroblast IFN gamma	0.7	1.5
93106 Dermal Fibroblasts CCD1070 resting	3.2	5.4
93361 Dermal Fibroblasts CCD1070 TNF alpha 4 ng/ml	1.9	14.9
93105 Dermal Fibroblasts CCD1070 IL-1 beta 1 ng/ml	5.7	1.4
93772 dermal fibroblast IFN gamma	1.0	0.0
93771 dermal fibroblast IL-4	0.4	2.6
93892 Dermal fibroblasts none	0.0	1.8
99202 Neutrophils TNFa+LPS	0.0	0.9

99203 Neutrophils none	2.9	2.4
735010 Colon normal	3.2	9.7
735019 Lung none	63.2	63.7
64028-1 Thymus none	23.0	40.1
64030-1 Kidney none	100.0	100.0

Panel 1 Summary: Ag147 Expression of the NOV8a gene is highest in testis (CT = 25.1). This gene is also highly to moderately expressed throughout the CNS, including in amygdala, cerebellum, hippocampus, substantia nigra, thalamus, hypothalamus and spinal cord, suggesting an important functional role in CNS processes. The NOV8a gene encodes a protein with homology to PAPIN, plakophilin-related armadillo repeat protein-interacting PSD-95/Dlg-A/ZO-1 (PDZ) protein. Ligands of PAPIN are thought to form a complex with p0071/NPRAP/ δ -catenin and presenilin 1 and may play roles in Notch or Wnt/Wingless pathways. Because presenilin is known to play a role in Alzheimer's disease, inhibitors of interactions between the NOV8A gene product and its biological interactors may be useful in the treatment of Alzheimer's disease or other diseases linked to the Wnt pathway, such as cancer or autism.

Lower levels of expression of the NOV8a gene are also seen in some metabolic tissues including pancreas, adrenal gland, pituitary gland, thyroid, heart, skeletal muscle and liver. Therefore, this gene may play a role in the development of diseases in any or all of these tissues.

Panel 1.2 Summary: Ag718 Results from three experiments using the same probe/primer set show only modest agreement. This discussion pertains to results seen in the majority of the experiments. Expression of the NOV8a gene is highest in heart and cerebral cortex. Thus, this gene could potentially be used to distinguish heart and cerebral cortex from other tissues. This gene is also highly to moderately expressed in other regions of the CNS, including spinal cord, hippocampus, amygdala, cerebellum, and thalamus. Please see Panel 1 summary for description of potential utility of this gene in the CNS.

Panel 2D Summary: Ag718 Results from three experiments using the same probe/primer set are in excellent agreement. Expression of the NOV8a gene in Panel 2D is highest in a sample derived from a kidney cancer. However, the predominant expression pattern in this panel is higher expression in normal tissues when compared to adjacent cancer tissues. This gene is expressed at lower levels 7 of 9 kidney cancers and 5 of 5 lung cancers

relative to the normal controls. Thus, expression of the NOV8a gene could be used to distinguish normal kidney or lung tissue from cancerous kidney or lung tissue and may have utility as a diagnostic marker. Finally, therapeutic modulation of this gene product might have benefit in the treatment of lung or kidney cancer.

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Panel 4D/4R Summary: Ag718 Results from three experiments using the same probe/primer set are in reasonable agreement. The NOV8a gene is expressed highly in keratinocytes treated with TNFa and IFNg. Significant expression of this gene is also seen in thymus, small airway epithelium and microvascular dermal endothelium treated with TNF-a and IL-1b. Therefore, antibodies against the protein encoded by the NOV8a gene might be useful in down modulating inflammatory responses observed in asthma, emphysema, skin diseases such as psoriasis, and contact hypersensitivity.

Panel 4.1D Summary: Ag3681/Ag4085 The NOV8a gene is expressed highly in keratinocytes treated with TNFa and IFNg, consistent with what is seen in Panels 4D/4R. Significant expression of this gene is also seen in lung microvascular endothelial cells treated with TNFa and IL-1b. Therefore, antibodies against the protein encoded by the NOV8a gene might be useful in down modulating inflammatory responses observed in asthma, emphysema, skin diseases such as psoriasis, and contact hypersensitivity.

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References:

1. Deguchi M., Iizuka T., Hata Y., Nishimura W., Hirao K., Yao I., Kawabe H., Takai Y. (2000) PAPIN. A novel multiple PSD-95/Dlg-A/ZO-1 protein interacting with neural plakophilin-related armadillo repeat protein/delta-catenin and p0071. J. Biol. Chem. 275:29875-29880.

A neural plakophilin-related armadillo repeat protein (NPRAP)/delta-catenin interacts with one of Alzheimer disease-related gene products, presenilin 1. Deguchi et al. have previously reported the interaction of NPRAP/delta-catenin with synaptic scaffolding molecule, which is involved in the assembly of synaptic components. NPRAP/delta-catenin also interacts with E-cadherin and beta-catenin and is implicated in the organization of cell-cell junctions. p0071, a ubiquitous isoform of NPRAP/delta-catenin, is localized at desmosomes in HeLa and A431 cells and at adherens junctions in Madin-Darby bovine kidney cells. Deguchi et al. have identified here a novel protein interacting with NPRAP/delta-catenin and p0071 and named this protein plakophilin-related armadillo repeat protein-interacting

PSD-95/Dlg-A/ZO-1 (PDZ) protein (PAPIN). PAPIN has six PDZ domains and binds to NPRAP/delta-catenin and p0071 via the second PDZ domain. PAPIN and p0071 are ubiquitously expressed in various tissues and are localized at cell-cell junctions in normal rat kidney cells and bronchial epithelial cells. PAPIN may be a scaffolding protein connecting components of epithelial junctions with p0071.

5
PMID: 10896674

10 2. Fraser P.E., Yu G., Levesque L., Nishimura M., Yang D.S., Mount H.T., Westaway D., St George-Hyslop P.H. (2001) Presenilin function: connections to Alzheimer's disease and signal transduction. Biochem. Soc. Symp. 67:89-100.

15 Missense mutations in presenilin 1 (PS1) and presenilin 2 (PS2) are associated with early-onset familial Alzheimer's disease which displays an accelerated deposition of amyloid plaques and neurofibrillary tangles. Presenilins are multi-spanning transmembrane proteins which localize primarily to the endoplasmic reticulum and the Golgi compartments. Fraser et al. have previously demonstrated that PS1 exists as a high-molecular-mass complex that is likely to contain several functional ligands. Potential binding proteins were screened by the yeast two-hybrid system using the cytoplasmically orientated PS1 loop domain which was shown to interact strongly with members of the armadillo family of proteins, including beta-catenin, p0071 and a novel neuron-specific plakophilin-related armadillo protein (NPRAP).

20 Armadillo proteins can have dual functions that encompass the stabilization of cellular junctions/synapses and the mediation of signal transduction pathways. These observations suggest that PS1 may contribute to both aspects of armadillo-related pathways involving neurite outgrowth and nuclear translocation of beta-catenin upon activation of the wingless (Wnt) pathway. Alzheimer's disease (AD)-related presenilin mutations exhibit a dominant gain of aberrant function resulting in the prevention of beta-catenin translocation following Wnt signalling. These findings indicate a functional role for PS1 in signalling and suggest that mistrafficking of selected presenilin ligands may be a potential mechanism in the genesis of AD.

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30

PMID: 11447843

3. Wassink T.H., Piven J., Vieland V.J., Huang J., Swiderski R.E., Pietila J., Braun T., Beck G., Folstein S.E., Haines J.L., Sheffield V.C. (2001) Evidence supporting WNT2 as an autism susceptibility gene. *Am. J. Med. Genet.* 105:406-413.

Wassink et al. examined WNT2 as a candidate disease gene for autism for the following reasons. First, the WNT family of genes influences the development of numerous organs and systems, including the central nervous system. Second, WNT2 is located in the region of chromosome 7q31-33 linked to autism and is adjacent to a chromosomal breakpoint in an individual with autism. Third, a mouse knockout of Dvl1, a member of a gene family essential for the function of the WNT pathway, exhibits a behavioral phenotype characterized primarily by diminished social interaction. Wassink et al. screened the WNT2 coding sequence for mutations in a large number of autistic probands and found two families containing nonconservative coding sequence variants that segregated with autism in those families. Wassink et al. also identified linkage disequilibrium (LD) between a WNT2 3'UTR SNP and a sample of autism-affected sibling pair (ASP) families and trios. The LD arose almost exclusively from a subgroup of ASP families defined by the presence of severe language abnormalities and was also found to be associated with the evidence for linkage to 7q from our previously published genomewide linkage screen. Furthermore, expression analysis demonstrated WNT2 expression in the human thalamus. Based on these findings, Wassink et al. hypothesize that rare mutations occur in the WNT2 gene that significantly increase susceptibility to autism even when present in single copies, while a more common WNT2 allele (or alleles) not yet identified may exist that contributes to the disorder to a lesser degree.

PMID: 11449391

25 4. De Ferrari G.V., Inestrosa N.C. (2000) Wnt signaling function in Alzheimer's disease. *Brain Res Brain Res Rev* 33:1-12.

Alzheimer's disease (AD) is a neurodegenerative disease with progressive dementia accompanied by three main structural changes in the brain: diffuse loss of neurons; 30 intracellular protein deposits termed neurofibrillary tangles (NFT) and extracellular protein deposits termed amyloid or senile plaques, surrounded by dystrophic neurites. Two major hypotheses have been proposed in order to explain the molecular hallmarks of the disease: The 'amyloid cascade' hypothesis and the 'neuronal cytoskeletal degeneration' hypothesis. While the former is supported by genetic studies of the early-onset familial forms of AD (FAD), the

latter revolves around the observation *in vivo* that cytoskeletal changes - including the abnormal phosphorylation state of the microtubule associated protein tau - may precede the deposition of senile plaques. Recent studies have suggested that the trafficking process of membrane associated proteins is modulated by the FAD-linked presenilin (PS) proteins, and
5 that amyloid beta-peptide deposition may be initiated intracellularly, through the secretory pathway. Current hypotheses concerning presenilin function are based upon its cellular localization and its putative interaction as macromolecular complexes with the cell-adhesion/signaling beta-catenin molecule and the glycogen synthase kinase 3beta (GSK-3beta) enzyme. Developmental studies have shown that PS proteins function as components in the
10 Notch signal transduction cascade and that beta-catenin and GSK-3beta are transducers of the Wnt signaling pathway. Both pathways are thought to have an important role in brain development, and they have been connected through Dishevelled (Dvl) protein, a known transducer of the Wnt pathway. In addition to a review of the current state of research on the subject, DeFerrari et al. present a cell signaling model in which a sustained loss of function of
15 Wnt signaling components would trigger a series of misrecognition events, determining the onset and development of AD.

PMID: 10967351

20 **Example 3. SNP analysis of NOVX clones**

SeqCalling™ Technology: cDNA was derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, cell lines, primary cells or tissue cultured primary cells and cell lines. Cells and cell lines may have been
25 treated with biological or chemical agents that regulate gene expression for example, growth factors, chemokines, steroids. The cDNA thus derived was then sequenced using CuraGen's proprietary SeqCalling technology. Sequence traces were evaluated manually and edited for corrections if appropriate. cDNA sequences from all samples were assembled with themselves and with public ESTs using bioinformatics programs to generate CuraGen's human SeqCalling
30 database of SeqCalling assemblies. Each assembly contains one or more overlapping cDNA sequences derived from one or more human samples. Fragments and ESTs were included as components for an assembly when the extent of identity with another component of the

assembly was at least 95% over 50 bp. Each assembly can represent a gene and/or its variants such as splice forms and/or single nucleotide polymorphisms (SNPs) and their combinations.

Variant sequences are included in this application. A variant sequence can include a single nucleotide polymorphism (SNP). A SNP can, in some instances, be referred to as a 5 "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA. A SNP can arise in several ways. For example, a SNP may be due to a substitution of one nucleotide for another at the polymorphic site. Such a substitution can be either a transition or a transversion. A SNP can also arise from a deletion of a nucleotide or an insertion of a nucleotide, relative to a reference allele. In this case, the polymorphic site is a site at which 10 one allele bears a gap with respect to a particular nucleotide in another allele. SNPs occurring within genes may result in an alteration of the amino acid encoded by the gene at the position of the SNP. Intragenic SNPs may also be silent, however, in the case that a codon including a SNP encodes the same amino acid as a result of the redundancy of the genetic code. SNPs occurring outside the region of a gene, or in an intron within a gene, do not result in changes in 15 any amino acid sequence of a protein but may result in altered regulation of the expression pattern for example, alteration in temporal expression, physiological response regulation, cell type expression regulation, intensity of expression, stability of transcribed message.

Method of novel SNP Identification: SNPs are identified by analyzing sequence assemblies using CuraGen's proprietary SNPTool algorithm. SNPTool identifies variation in 20 assemblies with the following criteria: SNPs are not analyzed within 10 base pairs on both ends of an alignment; Window size (number of bases in a view) is 10; The allowed number of mismatches in a window is 2; Minimum SNP base quality (PHRED score) is 23; Minimum number of changes to score an SNP is 2/assembly position. SNPTool analyzes the assembly 25 and displays SNP positions, associated individual variant sequences in the assembly, the depth of the assembly at that given position, the putative assembly allele frequency, and the SNP sequence variation. Sequence traces are then selected and brought into view for manual validation. The consensus assembly sequence is imported into CuraTools along with variant sequence changes to identify potential amino acid changes resulting from the SNP sequence variation. Comprehensive SNP data analysis is then exported into the SNPCalling database.

Method of novel SNP Confirmation: SNPs are confirmed employing a validated 30 method known as Pyrosequencing (Pyrosequencing, Westborough, MA). Detailed protocols for Pyrosequencing can be found in: Alderborn et al. Determination of Single Nucleotide Polymorphisms by Real-time Pyrophosphate DNA Sequencing. (2000). *Genome Research*. 10, Issue 8, August. 1249-1265. In brief, Pyrosequencing is a real time primer extension process

of genotyping. This protocol takes double-stranded, biotinylated PCR products from genomic DNA samples and binds them to streptavidin beads. These beads are then denatured producing single stranded bound DNA. SNPs are characterized utilizing a technique based on an indirect bioluminometric assay of pyrophosphate (PPi) that is released from each dNTP upon DNA chain elongation. Following Klenow polymerase-mediated base incorporation, PPi is released and used as a substrate, together with adenosine 5'-phosphosulfate (APS), for ATP sulfurylase, which results in the formation of ATP. Subsequently, the ATP accomplishes the conversion of luciferin to its oxi-derivative by the action of luciferase. The ensuing light output becomes proportional to the number of added bases, up to about four bases. To allow processivity of the method dNTP excess is degraded by apyrase, which is also present in the starting reaction mixture, so that only dNTPs are added to the template during the sequencing. The process has been fully automated and adapted to a 96-well format, which allows rapid screening of large SNP panels. The DNA and protein sequences for the novel single nucleotide polymorphic variants are reported. Variants are reported individually but any combination of all or a select subset of variants are also included. In addition, the positions of the variant bases and the variant amino acid residues are underlined.

Results

Variants are reported individually but any combination of all or a select subset of variants are also included as contemplated NOVX embodiments of the invention.

20

NOV1a SNP data:

NOV1a has two SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOS:1 and 2, respectively. The nucleotide sequence of the NOV1a variant differs as shown in Table 54.

25

Table 54. cSNP and Coding Variants for NOV1a				
NT Position of cSNP	Wild Type NT	Variant NT	Amino Acid position	Amino Acid Change
994	C	T	271	P->S
1707	A	G	508	No change

NOV7a SNP data:

NOV7a has four SNP variants, whose variant positions for its nucleotide and amino acid sequences is numbered according to SEQ ID NOS:X and Y, respectively. The nucleotide sequence of the NOV7a variant differs as shown in Table 55.

Table 55. cSNP and Coding Variants for NOV7a				
NT Position of cSNP	Wild Type NT	Variant NT	Amino Acid position	Amino Acid Change
1023	C	G	341	No change
1247	C	T	416	A->V

NOV8a SNP data:

5

NOV8a has one SNP variant, whose variant position for its nucleotide and amino acid sequences is numbered according to SEQ ID NOs:X and Y, respectively. The nucleotide sequence of the NOV8a variant differs as shown in Table 56.

Table 57. cSNP and Coding Variants for NOV8a				
NT Position of cSNP	Wild Type NT	Variant NT	Amino Acid position	Amino Acid Change
703	G	A	201	No change
4244	G	A	1381	No change

Example 4: SAGE analysis for NOV1

- Serial Analysis of Gene Expression, or SAGE, is an experimental technique designed to gain a quantitative measure of gene expression. The SAGE technique itself includes several 5 steps utilizing molecular biological, DNA sequencing and bioinformatics techniques. These steps (reviewed in Adams MD, "Serial analysis of gene expression: ESTs get smaller." Bioessays. 18(4):261-2 (1996)) have been used to produce 9 or 10 base "tags", which are then, in some manner, assigned gene descriptions. For experimental reasons, these tags are immediately adjacent to the 3' end of the 3'-most NlaIII restriction site in cDNA sequences.
- 10 The Cancer Genome Anatomy Project, or CGAP, is an NCI-initiated and sponsored project, which hopes to delineate the molecular fingerprint of the cancer cell. It has created a database of those cancer-related projects that used SAGE analysis in order to gain insight into the initiation and development of cancer in the human body. The SAGE expression profiles reported in this invention are generated by first identifying the Unigene accession ID
- 15 associated with the given MTC gene by querying the Unigene database at <http://www.ncbi.nlm.nih.gov/UniGene/>. This page has then a link to the SAGE : Gene to Tag mapping ([http://www.ncbi.nlm.nih.gov/SAGE/SAGEcid.cgi?cid="unigeneID"](http://www.ncbi.nlm.nih.gov/SAGE/SAGEcid.cgi?cid='unigeneID')).

This generated the reports that are included in this application, which list the number of tags found for the given gene in a given sample along with the relative expression. This 20 information is then used to understand whether the gene has a more general role in tumorogenesis and/or tumor progression. A list of the SAGE libraries generated by CGAP and used in the analysis can be found at <http://www.ncbi.nlm.nih.gov/SAGE/sagelb.cgi>.

UniGene cluster: Hs_255372

Hs_255372 : hypothetical protein DKFZp564O1278

SAGE library data and reliable tag summary:

Reliable tags found in SAGE libraries:

CTGAACCTGA	Library name	Tags per million	Tag counts	Total tags
	SAGE HCT116	16	1	60322
	SAGE Caco 2	18	1	61601
	SAGE Chen Tumor Pt	14	1	66304
	SAGE HX	83	3	32157
	SAGE H128	185	6	32420
	SAGE Duke H382	17	1	57529
	SAGE SW837	18	1	60988
	SAGERKO	96	5	52064
	SAGE PR317 normal prostate	16	1	59419
	SAGE NC1	19	1	50115
	SAGE Tu88	61	3	49005
	SAGE SciencePark MCF7 Control	18	1	61078
	SAGE LNCaP	44	1	22837
	SAGE OVT-7	18	1	54814
	SAGE MDA453	62	1	18924
	SAGE mammary epithelium	20	1	49167
	SAGE OVT-8	29	1	33575
	SAGE Duke-H988	35	1	28015

Reliable tags NOT found in SAGE libraries:

OTHER EMBODIMENTS

Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims, which follow. In particular, it is
5 contemplated by the inventors that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims. The choice of nucleic acid starting material, clone of interest, or library type is believed to be a matter of routine for a person of ordinary skill in the art with knowledge of the embodiments described herein. Other aspects, advantages, and modifications considered to be
10 within the scope of the following claims.

WHAT IS CLAIMED IS:

1. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:
 - (a) a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 27;
 - (b) a variant of a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 27, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of the amino acid residues from the amino acid sequence of said mature form;
 - (c) an amino acid sequence selected from the group consisting SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 27; and
 - (d) a variant of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 27, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of amino acid residues from said amino acid sequence.
2. The polypeptide of claim 1, wherein said polypeptide comprises the amino acid sequence of a naturally-occurring allelic variant of an amino acid sequence selected from the group consisting SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 27.
3. The polypeptide of claim 2, wherein said allelic variant comprises an amino acid sequence that is the translation of a nucleic acid sequence differing by a single nucleotide from a nucleic acid sequence selected from the group consisting of SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26.
4. The polypeptide of claim 1, wherein the amino acid sequence of said variant comprises a conservative amino acid substitution.

5. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group consisting of:
 - (a) a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 27;
 - (b) a variant of a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 27, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of the amino acid residues from the amino acid sequence of said mature form;
 - (c) an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 27;
 - (d) a variant of an amino acid sequence selected from the group consisting SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 27, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of amino acid residues from said amino acid sequence;
 - (e) a nucleic acid fragment encoding at least a portion of a polypeptide comprising an amino acid sequence chosen from the group consisting of SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 27, or a variant of said polypeptide, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of amino acid residues from said amino acid sequence; and
 - (f) a nucleic acid molecule comprising the complement of (a), (b), (c), (d) or (e).
6. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule comprises the nucleotide sequence of a naturally-occurring allelic nucleic acid variant.
7. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule encodes a polypeptide comprising the amino acid sequence of a naturally-occurring polypeptide variant.

8. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule differs by a single nucleotide from a nucleic acid sequence selected from the group consisting of SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26.
9. The nucleic acid molecule of claim 5, wherein said nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of:
 - (a) a nucleotide sequence selected from the group consisting of SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26;
 - (b) a nucleotide sequence differing by one or more nucleotides from a nucleotide sequence selected from the group consisting of SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, provided that no more than 20% of the nucleotides differ from said nucleotide sequence;
 - (c) a nucleic acid fragment of (a); and
 - (d) a nucleic acid fragment of (b).
10. The nucleic acid molecule of claim 5, wherein said nucleic acid molecule hybridizes under stringent conditions to a nucleotide sequence chosen from the group consisting SEQ ID NOS:1, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, and 26, or a complement of said nucleotide sequence.
11. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of:
 - (a) a first nucleotide sequence comprising a coding sequence differing by one or more nucleotide sequences from a coding sequence encoding said amino acid sequence, provided that no more than 20% of the nucleotides in the coding sequence in said first nucleotide sequence differ from said coding sequence;
 - (b) an isolated second polynucleotide that is a complement of the first polynucleotide; and
 - (c) a nucleic acid fragment of (a) or (b).
12. A vector comprising the nucleic acid molecule of claim 11.
13. The vector of claim 12, further comprising a promoter operably-linked to said nucleic acid molecule.

14. A cell comprising the vector of claim 12.
15. An antibody that binds immunospecifically to the polypeptide of claim 1.
16. The antibody of claim 15, wherein said antibody is a monoclonal antibody.
17. The antibody of claim 15, wherein the antibody is a humanized antibody.
18. A method for determining the presence or amount of the polypeptide of claim 1 in a sample, the method comprising:
 - (a) providing the sample;
 - (b) contacting the sample with an antibody that binds immunospecifically to the polypeptide; and
 - (c) determining the presence or amount of antibody bound to said polypeptide, thereby determining the presence or amount of polypeptide in said sample.
19. A method for determining the presence or amount of the nucleic acid molecule of claim 5 in a sample, the method comprising:
 - (a) providing the sample;
 - (b) contacting the sample with a probe that binds to said nucleic acid molecule; and
 - (c) determining the presence or amount of the probe bound to said nucleic acid molecule,thereby determining the presence or amount of the nucleic acid molecule in said sample.
20. The method of claim 19 wherein presence or amount of the nucleic acid molecule is used as a marker for cell or tissue type.
21. The method of claim 20 wherein the cell or tissue type is cancerous.
22. A method of identifying an agent that binds to a polypeptide of claim 1, the method comprising:
 - (a) contacting said polypeptide with said agent; and
 - (b) determining whether said agent binds to said polypeptide.

23. The method of claim 22 wherein the agent is a cellular receptor or a downstream effector.
24. A method for identifying an agent that modulates the expression or activity of the polypeptide of claim 1, the method comprising:
 - (a) providing a cell expressing said polypeptide;
 - (b) contacting the cell with said agent, and
 - (c) determining whether the agent modulates expression or activity of said polypeptide,whereby an alteration in expression or activity of said peptide indicates said agent modulates expression or activity of said polypeptide.
25. A method for modulating the activity of the polypeptide of claim 1, the method comprising contacting a cell sample expressing the polypeptide of said claim with a compound that binds to said polypeptide in an amount sufficient to modulate the activity of the polypeptide.
26. A method of treating or preventing a NOVX-associated disorder, said method comprising administering to a subject in which such treatment or prevention is desired the polypeptide of claim 1 in an amount sufficient to treat or prevent said NOVX-associated disorder in said subject.
27. The method of claim 26 wherein the disorder is selected from the group consisting of cardiomyopathy and atherosclerosis.
28. The method of claim 26 wherein the disorder is related to cell signal processing and metabolic pathway modulation.
29. The method of claim 26, wherein said subject is a human.
30. A method of treating or preventing a NOVX-associated disorder, said method comprising administering to a subject in which such treatment or prevention is desired the nucleic acid of claim 5 in an amount sufficient to treat or prevent said NOVX-associated disorder in said subject.

31. The method of claim 30 wherein the disorder is selected from the group consisting of cardiomyopathy and atherosclerosis.
32. The method of claim 30 wherein the disorder is related to cell signal processing and metabolic pathway modulation.
33. The method of claim 30, wherein said subject is a human.
34. A method of treating or preventing a NOVX-associated disorder, said method comprising administering to a subject in which such treatment or prevention is desired the antibody of claim 15 in an amount sufficient to treat or prevent said NOVX-associated disorder in said subject.
35. The method of claim 34 wherein the disorder is diabetes.
36. The method of claim 34 wherein the disorder is related to cell signal processing and metabolic pathway modulation.
37. The method of claim 34, wherein the subject is a human.
38. A pharmaceutical composition comprising the polypeptide of claim 1 and a pharmaceutically-acceptable carrier.
39. A pharmaceutical composition comprising the nucleic acid molecule of claim 5 and a pharmaceutically-acceptable carrier.
40. A pharmaceutical composition comprising the antibody of claim 15 and a pharmaceutically-acceptable carrier.
41. A kit comprising in one or more containers, the pharmaceutical composition of claim 38.
42. A kit comprising in one or more containers, the pharmaceutical composition of claim 39.

43. A kit comprising in one or more containers, the pharmaceutical composition of claim 40.
44. A method for determining the presence of or predisposition to a disease associated with altered levels of the polypeptide of claim 1 in a first mammalian subject, the method comprising:
 - (a) measuring the level of expression of the polypeptide in a sample from the first mammalian subject; and
 - (b) comparing the amount of said polypeptide in the sample of step (a) to the amount of the polypeptide present in a control sample from a second mammalian subject known not to have, or not to be predisposed to, said disease;
wherein an alteration in the expression level of the polypeptide in the first subject as compared to the control sample indicates the presence of or predisposition to said disease.
45. The method of claim 44 wherein the predisposition is to a cancer.
46. A method for determining the presence of or predisposition to a disease associated with altered levels of the nucleic acid molecule of claim 5 in a first mammalian subject, the method comprising:
 - (a) measuring the amount of the nucleic acid in a sample from the first mammalian subject; and
 - (b) comparing the amount of said nucleic acid in the sample of step (a) to the amount of the nucleic acid present in a control sample from a second mammalian subject known not to have or not be predisposed to, the disease;
wherein an alteration in the level of the nucleic acid in the first subject as compared to the control sample indicates the presence of or predisposition to the disease.
47. The method of claim 46 wherein the predisposition is to a cancer.
48. A method of treating a pathological state in a mammal, the method comprising administering to the mammal a polypeptide in an amount that is sufficient to alleviate the pathological state, wherein the polypeptide is a polypeptide having an amino acid sequence at least 95% identical to a polypeptide comprising an amino acid sequence of at least one of SEQ ID NOS:2, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, and 27, or a biologically active fragment thereof.

49. A method of treating a pathological state in a mammal, the method comprising administering to the mammal the antibody of claim 15 in an amount sufficient to alleviate the pathological state.

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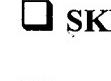
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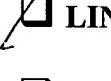
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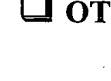
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